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From: Bunner, Bridget  
Sent: Monday, March 08, 2004 11:59 AM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Hi! I'd like to request a sequence search for case 09/555,296:

1. the amino acid sequence of SEQ ID NO: 4

Thanks!

Bridget Bunner

*Art Unit 1647  
Rem 4C65  
(571) 272-0881  
mailbox 4C70*

*CR/CH*

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: March 9, 2004, 13:32:25 ; Search time 23 seconds

(without alignments)

469.123 Million cell updates/sec

Title: US-09-555-296B-4

Perfect score: 1125

Sequence: 1 MKMQVVLITFVSAALATOA. .... DRKTYDIFNEBCVYNGEPWL 2.09

Scoring table: BIOSUM62

Gapp 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : ISSUED\_PATENTS\_AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB\_pep:\*

2: /cgn2\_6/ptodata/2/iaa/5B\_COMB\_pep:\*

3: /cgn2\_6/ptodata/2/iaa/6A\_COMB\_pep:\*

4: /cgn2\_6/ptodata/2/iaa/6B\_COMB\_pep:\*

5: /cgn2\_6/ptodata/2/iaa/PCMS\_COMB\_pep:\*

6: /cgn2\_6/ptodata/2/iaa/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1125	100.0	209	4 US-09-618-919A-22
2	290.5	25.8	190	4 US-09-618-919A-18
3	265	23.6	200	4 US-09-618-919A-20
4	252	22.4	190	4 US-09-618-919A-16
5	102.5	28.4	190	4 US-09-134-000C-3594
6	91	8.1	202	1 US-07-807-022A-1
7	84.5	7.5	497	4 US-09-107-532A-5279
8	83	7.4	510	4 US-09-134-000C-6335
9	83	7.4	2285	4 US-09-308-375-2
10	81	7.2	659	3 US-08-894-810B-1
11	81	7.2	3	US-08-894-810B-5
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14	79.5	7.1	913	2 US-08-470-435-5
15	79.5	7.1	913	2 US-08-339-483-5
16	79.5	7.1	913	2 US-08-470-373-5
17	79.5	7.1	913	3 US-08-470-671-5
18	79.5	7.1	913	3 US-08-483-572A-5
19	79.5	7.1	913	3 US-08-897-438-5
20	79.5	7.1	913	4 US-08-637-654-11
21	79.5	7.1	913	4 US-08-649-518-11
22	78	6.9	1871	3 US-09-349-546-1
23	78	6.9	1871	4 US-09-502-831-1
24	78	6.9	1871	4 US-09-489-038-12461
25	77.5	6.9	652	4 US-08-489-038-12461
26	77	6.8	640	4 US-08-328-352A-8058
27	6.8	6.8	914	1 US-09-618-919A-18

ALIGNMENTS

RESULT 1

US-09-18-919A-22

; Sequence 22, Appl

; Patent No. 6617312

; GENERAL INFORMATION:

; APPLICANT: Pasen, Guido Christiaan

; TITLE OF INVENTION: Vasoactive Amine Binding Molecules

; FILE REFERENCE: 2369-1-0101CN

; CURRENT APPLICATION NUMBER: US/09-618, 919A

; CURRENT FILING DATE: 2000-07-18

; PRIOR APPLICATION NUMBER: US 09/180, 733

; PRIOR FILING DATE: 1998-11-13

; PRIOR APPLICATION NUMBER: GB 9610484.0

; PRIOR FILING DATE: 1996-05-18

; PRIOR APPLICATION NUMBER: GB 9707844.8

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 22

; LENGTH: 209

; TYPE: PRT

; ORGANISM: Dermacentor reticulatus

US-09-618-919A-22

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Best Local Similarity 100.0%; Pred. No. 2.0e-114; DB

Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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PRIOR FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 3594  
 LENGTH: 284  
 TYPE: PRT  
 ORGANISM: *Enterococcus faecalis*  
 US-09-134-000C-3594

Query Match 9.1%; Score 102.5; DB 4; Length 284;  
 Best Local Similarity 26.9%; Pred. No. 0.0065; Mismatches 82; Indels 60; Gaps 11;  
 Matches 60; Conservative 26; Mismatches 72; Indels 65; Gaps 15;

Qy 16 LATORETISA----KAGENPLWAHELLIGKQDAWAKSI-DOGVSYTIVLAKTY---- 64  
 Db 68 LVGDKEETSSYGFAVKKGQNP----BLIKKENAGLNLKONG---TYDKILNNVLTAGD 119

Qy 65 ENDGGSWSQPKCILQVQETERKEEDYTWSVTFRWASSPRTKVNW----TEVKA 116  
 Db 120 BINTQDAGQMK---KTPKKEKTYIASDSTP---APPFEQNQGDVYGLDULVR 170

Qy 117 V-----FOY-GYKINIRALEY-QVGG--GLNITDTLIFTPOBLCDVYFYVENDOG 162  
 Db 171 AAEQGFTVEPKF1GQSSAVQAVESQGADGVAGM1TD----DRKKARDFSFVYFDSG 225

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RESULT 6  
 US-07-807-022A-1  
 Sequence 1, Application US/07807022A  
 Patent No. 5321010  
 GENERAL INFORMATION:  
 APPLICANT: Connolly, Thomas M.  
 APPLICANT: Neepur, Michael  
 APPLICANT: Waxman, Lloyd  
 TITLE OF INVENTION: Protein for Inhibiting Adhesion of  
 TITLE OF INVENTION: Platelets to Collagen  
 NUMBER OF SEQUENCES: 2  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Merck & Co., Inc.  
 STREET: P. O. Box 2000  
 CITY: Rahway  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 08840  
 COMPUTER READABLE FORM:  
 COMPUTER TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/07/807,022A  
 FILING DATE: 1991-12-10  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Parr, Richard S.  
 REGISTRATION NUMBER: 32,586  
 REFERENCE/DOCKET NUMBER: 18143  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (908) 594-4958  
 TELEFAX: 908-594-4720  
 TEL: 138825  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 202 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: unknown  
 TOPOLOGY: unknown  
 MOLECULE TYPE: protein  
 US-07-807-022A-1

RESULT 7  
 US-09-107-532A-5279  
 Sequence 5279, Application US/09107332A  
 Patent No. 6553275  
 GENERAL INFORMATION:  
 APPLICANT: Lynn A. doucette-stamm and David Bush  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 NUMBER OF SEQUENCES: 7310  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
 STREET: 100 Beaver Street  
 CITY: Waltham  
 STATE: Massachusetts  
 COUNTRY: USA  
 ZIP: 02454  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: CD/ROM ISO9660  
 COMPUTER: PC  
 OPERATING SYSTEM: <Unknown>  
 SOFTWARE: ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/107,532A  
 FILING DATE: 30-Jun-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 6/0085,598  
 FILING DATE: 14 May 1998  
 APPLICATION NUMBER: 60/051571  
 FILING DATE: JULY 2, 1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Arinelli, Pamela Deneke  
 REGISTRATION NUMBER: 40,489  
 REFERENCE/DOCKET NUMBER: GTC-012  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (781) 891-5007  
 TELEFAX: (781) 893-6277  
 INFORMATION FOR SEQ ID NO: 5279:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 97 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 HYPOTHETICAL: YES  
 ORIGINAL SOURCE:  
 ORGANISM: *Enterococcus faecium*  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (B) LOCATION 1..497  
 SEQUENCE DESCRIPTION: SEQ ID NO: 5279:  
 US-09-107-532A-5279

Query Match      7.5%; Score 84.5; DB 4; Length 497;  
 Best Local Similarity 22.6%; Pred. No. 1.4;  
 Matches 47; Conservative 29; Mismatches 85; Indels 47; Gaps 9;

QY      26 KAGENPLWAHEBLLGKQDANKSIDQGSVYVLAKKTYEND--TGSNGSOKCQVQBI 83  
 Db      15 KPGEGTNGGATRANQEGAWDVKDQKLSISDVY--TDSURKEKTDQWMMHQV 71

QY      84 ERKEDDYTVTSPTFERNASSPIKYKNTVETKAVQYQYNTVRAIBQVG3GINTDYL 143  
 Db      72 KRAQDP--NSKYYPRGHNDPYHFKEDDIRLFAEMGFCKYRMSIAN-----TR 118

QY      144 IR-----TDGLCDVYVYRDAO---GELWVKSHY-----KAVPD 177

Db      119 IFPHGDEBTPNTEAGLFFPYDQVDECILKGYIBPVVNLSHYEMPLVLYTEYGGWPNRKUJQF 178

QY      178 YTFPVFVNFCAKDRKTI-YDIFNE ECV 202

Db      179 YTFPVFVNFCAKDRKTI-YDIFNE ECV 206

RESULT 8  
 US-09-134-000C-6635 Application US/09134000C  
 ; Sequence 6635; Application US/09134000C  
 ; Patent No. 6617156

GENERAL INFORMATION:  
 ; APPLICANT: LYNN Doucette-Stamm et al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
 ; TITLE OF INVENTION: ENTEROCOCCUS FABCALS FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 032795-1  
 ; CURRENT APPLICATION NUMBER: US/09/134,000C  
 ; CURRENT FILING DATE: 1998-08-13  
 ; PRIOR APPLICATION NUMBER: US 60/055,778  
 ; PRIOR FILING DATE: 1997-08-15  
 ; NUMBER OF SEQ ID NOS: 6812  
 ; SOFTWARE: Patentin version 3.1  
 ; SEQ ID NO: 6635  
 ; LENGTH: 510  
 ; ORGANISM: Enterococcus faecalis  
 ; US-09-134-000C-6635

Query Match      7.4%; Score 83; DB 4; Length 2285;  
 Best Local Similarity 23.3%; Pred. No. 19; Mismatches 79; Indels 62; Gaps 10;

QY      6 VLLITFVSAALAOETASAKAGENPLWAHEBLLGKQDANKSID--QGVAVTYVLAKT 63  
 Db      743 LIVSITVGGAFALG-----WALESILSSAAKAKDPEQSCQNTVAIIT 790

QY      64 YENDGSGWSQKQLOVQBIERKEDDYTVTSPTFERNASSPIKYKNTVETKAVFO--Y 120  
 Db      791 NRKSTDKLIQK-----BLQKKESERLS-----DEOELQVLTQIAQQTFLAVK 838

QY      121 GY-----ENIRVATEYQVGGGNITDYLIFDGECDVYPVNAQDGCELVWKK 169  
 Db      839 GYDSQGNATLTKTELEKALE-----NTKSYALKKQETRISAKKTFEDASKE--IKK 889

QY      170 S----HYKHPVQYCTFVNFCAKDRKTYDNEECY 203

Db      890 SKDELQKQYQIAVDND-----KGRPKWDLIADDYY 920

RESULT 10  
 US-09-894-818B-1  
 ; Sequence 1; Application US/08894818B  
 ; Patent No. 6261822

GENERAL INFORMATION:  
 ; APPLICANT: TAKAKURA, Hikaru  
 ; APPLICANT: MORISHITA, Mio  
 ; APPLICANT: YAMAMOTO, Katsuhiko  
 ; APPLICANT: MITTA, Masanori  
 ; APPLICANT: ASADA, Kiyozo  
 ; APPLICANT: TSUNASHWA, Subumu  
 ; APPLICANT: KATO, Ikunobu  
 ; TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES  
 ; NUMBER OF SEQUENCES: 42  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Brodwy and Neimark  
 ; STREET: 419 Seventh Street N.W., Ste. 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: United States of America  
 ; ZIP: 20004

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP96/03253  
 FILING DATE: 07-NOV-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/894,818B  
 FILING DATE: 20-MAY-1998  
 CLASSIFICATION: 45  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/JP96/03253  
 FILING DATE: 07-NOV-1996  
 APPLICATION NUMBER: JP 323285/1995  
 FILING DATE: 12-DEC-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Brodwy, Roger L.

RESULT 9  
 US-09-008-375-2  
 ; Sequence 2; Application US/09308375  
 ; Patent No. 630117  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genencor International, Inc.

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; REFERENCE/DOCKET NUMBER: 25, 618
; REFERENCE/DOCKET NUMBER: TAKAKURA=1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-1917
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 659 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-894-818B-1

Query Match 7.2%; Score 81; DB 3; Length 659;
Best Local Similarity 25.9%; Pred. No. 5; Mismatches 53; Conservative 20; Indels 70; Gaps 13;
Matches 53; Conservatve 20; Mismatches 62; Indels 70; Gaps 13;

Qy 41 KYODAWK-----SIDQGSV-TYVLAKTYENDTGSW--GSQPKCLOQOEIERKEDYT 91
Db 436 KYDDAKLTFTGSVALDKGSATHTFDVSGATFVTATLYWDGSSDIDLYDPNGNEVDYS 495
Qy 92 VTSVPTFRNASSPPIKYNTV--TVKAVQFGQYKNIRNALEYQV-----GGG- 136
Db 496 YTAYYGFKEK---VGYNPTAGTWTKVW--SYKGAAN--YQDVVSDGSLSQSGGN 545
Qy 137 -----LNITDTLIFTDGLCDVYFVNPNAQGCELWVKSHYKHPDYCTFVNVC 187
Db 546 PNPNPNPNPPTPTDQTFT-GSND--YWTSD-----TFTMNWS 583
Qy 188 AKDRKYD1----FNEECVNGEP 207
Db 584 GATKIKGDLTPDTSYNDLILYDP 608

RESULT 11
US-08-894-818B-5
; Sequence 5, Application US/08894818B
; Patent No. 6261822
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: YAMAMOTO, Katsuhiko
; APPLICANT: MITTA, Masanori
; APPLICANT: ASADA, Kiyozo
; APPLICANT: TSUNASAWA, Shusumu
; APPLICANT: KATO, Ikuo
; TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brody and Neimark
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States of America
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC/POS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/894,818B
; FILING DATE: 20-MAY-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/03253
; FILING DATE: 07-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 323285/1995
; FILING DATE: 12-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brody, Roger L.

RESULT 12
US-09-445-472-12
; Sequence 12, Application US/09145472
; Patent No. 6358226
; GENERAL INFORMATION:
; APPLICANT: TAKAKURA, Hikaru
; APPLICANT: MORISHITA, Mio
; APPLICANT: SHIMOJO, Tomoko
; APPLICANT: ASADA, Kiyozo
; APPLICANT: KATO, Ikuo
; TITLE OF INVENTION: SYSTEM FOR EXPRESSION HYPERTHERMOSTABLE
; FILE REFERENCE: TAKAKURA-6
; CURRENT APPLICATION NUMBER: US/09/445,472
; CURRENT FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 151969/1997
; PRIOR FILING DATE: 1997-06-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Thermococcus celar
; US-09-445-472-12

Query Match 7.2%; Score 81; DB 4; Length 659;
Best Local Similarity 25.9%; Pred. No. 5; Mismatches 53; Conservative 20; Indels 70; Gaps 13;
Matches 53; Conservatve 20; Mismatches 62; Indels 70; Gaps 13;

Qy 41 KYODAWK-----SIDQGSV-TYVLAKTYENDTGSW--GSQPKCLOQOEIERKEDYT 91
Db 436 KYDDAKLTFTGSVALDKGSATHTFDVSGATFVTATLYWDGSSDIDLYDPNGNEVDYS 495
Qy 92 VTSVPTFRNASSPPIKYNTV--TVKAVQFGQYKNIRNALEYQV-----GGG- 136
Db 496 YTAYYGFKEK---VGYNPTAGTWTKVW--SYKGAAN--YQDVVSDGSLSQSGGN 545
Qy 137 -----LNITDTLIFTDGLCDVYFVNPNAQGCELWVKSHYKHPDYCTFVNVC 187

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RESULT 13  
 US-08-487-890A-5  
 ; Sequence 5, Application US/08487890A  
 ; Patent No. 5708149

GENERAL INFORMATION:  
 APPLICANT: Doosmore, Sheena  
 APPLICANT: Harkness, Robin  
 APPLICANT: Schryvers, Anthony  
 APPLICANT: Chong, Pele  
 APPLICANT: Gray-Owen, Scott  
 APPLICANT: Yang, Yan-Ping  
 APPLICANT: Murdin, Andrew  
 APPLICANT: Klein, Michael

TITLE OF INVENTION: Transferrin Receptor Genes  
 NUMBER OF SEQUENCES: 147  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: 6th Floor, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/487,890A  
 FILING DATE: 07-JUN-1993  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/175,116  
 FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/148,968  
 FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 913 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-487-890A-5

Query Match  
 Best Local Similarity 21.9%; Pred. No. 12; DB 1; Length 913;  
 Matches 48; Conservative 32; Mismatches 60; Indels 79; Gaps 13;

QY 11 FVSAALATOQETTSAKAGENPFLWAHEELIGKVQD-AWKS-----IDQGVSVTVLAKTY 64  
 DB 593 YVNLIGLIGMRYDVSRKANESTI-----SVGKERNFSWNTGIVKPTPEWLDLISYRIS-TGF 646  
 647 RNPSPFAEMYGMWYGGKTDVWIGKFK---PETSRIQEFGLALKGDFGNIBISHFSNA-- 700

QY 104 PIKVVNVETVKAFFQ-----IGKVNNAIAEKGVGGNLTIDLIFDGEGLDVFY 155

RESULT 14  
 US-08-478-435-5  
 ; Sequence 5, Application US/08478435  
 ; Patent No. 5923233

GENERAL INFORMATION:  
 APPLICANT: Doosmore, Sheena  
 APPLICANT: Harkness, Robin  
 APPLICANT: Schryvers, Anthony  
 APPLICANT: Chong, Pele  
 APPLICANT: Gray-Owen, Scott  
 APPLICANT: Yang, Yan-Ping  
 APPLICANT: Murdin, Andrew  
 APPLICANT: Klein, Michael

TITLE OF INVENTION: Transferrin Receptor Genes  
 NUMBER OF SEQUENCES: 147  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Sim & McBurney  
 STREET: Suite 701, 330 University Avenue  
 CITY: Toronto  
 STATE: Ontario  
 COUNTRY: Canada  
 ZIP: MSG 1R7

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/478,435  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/337,483  
 FILING DATE: 08-NOV-1994  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/175,116  
 FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/148,968  
 FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:  
 NAME: Stewart, Michael I  
 REGISTRATION NUMBER: 24,973  
 REFERENCE/DOCKET NUMBER: 1038-462 MIS:wg

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (416) 595-1155  
 TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 913 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-478-435-5

Query Match  
 Best Local Similarity 21.9%; Pred. No. 12; DB 2; Length 913;  
 Matches 48; Conservative 32; Mismatches 60; Indels 79; Gaps 13;

QY 11 FVSAALATOQETTSAKAGENPFLWAHEELIGKVQD-AWKS-----IDQGVSVTVLAKTY 64  
 DB 593 YVNLIGLIGMRYDVSRKANESTI-----SVGKERNFSWNTGIVKPTPEWLDLISYRIS-TGF 646  
 647 RNPSPFAEMYGMWYGGKTDVWIGKFK---PETSRIQEFGLALKGDFGNIBISHFSNA-- 700

QY 104 PIKVVNVETVKAFFQ-----IGKVNNAIAEKGVGGNLTIDLIFDGEGLDVFY 155

Db 647 RNPSFAEMYGWRYGGKDTDVYIGFK---PETSRNQEGFLALKGDPGNEISHFSNA-- 700  
 QY 104 PIKYVNTETVKAVPQ-----YSYKNTIRNAIEVQVGGGLNTTDLIFDGLCDVY 155  
 Db 701 --YRNLIAFABEELSKNGTTGKGNY3FHNAQAKLV---GVNITAQDENG----- 745  
 QY 156 VPNAQGCELWVKSHYKHVPD--YCTFVFNFCAKDRK 192  
 Db 746 -----LW-----KRIPYGWTAFAYNRVVKVQDK 769

QY 156 VPNAQGCELWVKSHYKHVPD--YCTFVFNFCAKDRK 192  
 Db 746 -----LW-----KRIPYGWTAFAYNRVVKVQDK 769  
 Search completed: March 9, 2004, 13:36:04  
 Job time : 25 Secs

RESULT 15  
 US-08-337-483-5  
 ; Sequence 5, Application US/08337483  
 ; Patent No. 5922562  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Doosmore, Sheena  
 ; APPLICANT: Harkness, Robin  
 ; APPLICANT: Schryvers, Anthony  
 ; APPLICANT: Chong, Pele  
 ; APPLICANT: Gray-Owen, Scott  
 ; APPLICANT: Yang, Yan-ping  
 ; APPLICANT: Murdin, Andrew  
 ; APPLICANT: Klein, Michel  
 ; TIME OF INVENTION: Transferrin Receptor Gene  
 ; NUMBER OF SEQUENCES: 147  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Sim & McBurney  
 ; STREET: Suite 701, 330 University Avenue  
 ; CITY: Toronto  
 ; STATE: Ontario  
 ; COUNTRY: Canada  
 ; ZIP: MSG 1R7  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/337,483  
 ; FILING DATE: 08-NOV-1994  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Stewart, Michael I  
 ; REGISTRATION NUMBER: 24,973  
 ; REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (416) 595-1155  
 ; TELEFAX: (416) 595-1163  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 913 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; US-08-337-483-5

Query Match 7.1%; Score 79.5; DB 2; Length 913;  
 best local Similarity 21.9%; Pred. No. 12; Mismatches 13;  
 Matches 48; Conservative 32; Misnatches 60; Indels 79; Gaps 13;

QY 11 FVSAALATOETSAKAGENPLWAHEELIGKQD-AWKS-----IDQGVSVTYVAKTY 64  
 Db 593 YMDAGIGMREIDVSRKANBTT---SVGKFKAESNTGIVKPFEWLDSKRLS-TGF 646  
 QY 65 EN-----DRGSWSQFKCLOVQIERKE-----DVTYVSVFTRNASS 103  
 Db 647 RNPSFAEMYGWRYGGKDTDVYIGFK---PETSRNQEGFLALKGDPGNEISHFSNA-- 700  
 QY 104 PIKYVNTETVKAVPQ-----YSYKNTIRNAIEVQVGGGLNTTDLIFDGLCDVY 155  
 Db 701 --YRNLIAFABEELSKNGTTGKGNY3FHNAQAKLV---GVNITAQDENG----- 745

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 9, 2004, 13:33:35 ; Search time 33 Seconds (without alignment) Million cell updates/sec 1337.304 Million cell updates/sec

Title: perfect score: US-09-555-296B-4

Sequence: 1125 MRQMVVLLTFTVSAAATQAA.....DRKTYDIFNRCVQVNGPWL 209

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen Parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : Published Applications AA:\*

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2: /cgn2\_6/ptodata/1/pupbaa/PCTN\_NEW\_PUB\_Pep:\*

3: /cgn2\_6/ptodata/1/pupbaa/US06\_PUBCOMB.pep:\*

4: /cgn2\_6/ptodata/1/pupbaa/US07\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/1/pupbaa/US07\_PUBCOMB.pep:\*

6: /cgn2\_6/ptodata/1/pupbaa/PCTN\_NEW\_PUB\_Pep:\*

7: /cgn2\_6/ptodata/1/pupbaa/US08\_PUBCOMB.pep:\*

8: /cgn2\_6/ptodata/1/pupbaa/US07\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/1/pupbaa/US07\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/1/pupbaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/1/pupbaa/US10\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/1/pupbaa/US10\_PUBCOMB.pep:\*

13: /cgn2\_6/ptodata/1/pupbaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/1/pupbaa/US10\_PUBCOMB.pep:\*

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18: /cgn2\_6/ptodata/1/pupbaa/US10\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	282	25.1	171	US-10-085-572-7
2	282	25.1	171	US-10-087-195-7
3	251.5	22.4	182	US-10-085-572-8
4	251.5	22.4	182	US-10-087-195-8
5	239	21.2	172	US-10-085-572-6
6	239	21.2	172	US-10-087-195-6
7	102.5	9.1	722	US-09-815-242-10796
8	97.5	8.7	221	US-09-728-914-4
9	84	7.5	217	US-09-728-914-22
10	83	7.4	2285	9 US-09-312-183A-2
11	82	7.3	381	15 US-10-369-193-5686
12	81	7.2	627	16 US-10-389-566-2357
13	81	7.2	659	13 US-10-090-624-12
14	80.5	7.2	738	14 US-10-291-583-83
15	79.5	7.1	738	14 US-10-291-583-92

RESULT 1

US-10-085-572-7

; Sequence 7, Application US/10085572

; Publication No. US20020155499A1

; GENERAL INFORMATION:

; APPLICANT: Nuttall, Patricia, Ann

; APPLICANT: Paesen, Guido, Christian

; TITLE OF INVENTION: Treatment of Conjunctivitis

; FILE REFERENCE: 248-B-003

; CURRENT APPLICATION NUMBER: US-10-085-572

; CURRENT FILING DATE: 2003-02-27

; PRIOR APPLICATION NUMBER: PCT/GB00/03282

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: 9320674.0

; PRIOR FILING DATE: 1999-09-01

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FASTSEQ for Windows Version 4.0

; SEQ ID NO: 7

; LENGTH: 171

; TYPE: PRT

; ORGANISM: FS-HBP 2

; Query Match 25.1%; Score 222; DB 13; Length 171; Best Local Similarity 37.5%; Pred. No. 1; 4peptide; Matches 66; Conservative 29; Mismatches 69; Indels 12; Gaps 8;

Sequence 95, Appli

Sequence 2, Appli

Sequence 5, Appli

Sequence 87, Appli

Sequence 80, Appli

Sequence 5064, Appli

Sequence 113, Appli

Sequence 86, Appli

Sequence 90, Appli

Sequence 79, Appli

Sequence 81, Appli

Sequence 84, Appli

Sequence 85, Appli

Sequence 91, Appli

Sequence 94, Appli

Sequence 7764, AP

Sequence 11, Appli

Sequence 18, Appli

Sequence 3622, AP

Sequence 82, Appli

Sequence 749, App

Sequence 11803, A

Sequence 56, Appli

Sequence 99, Appli

Sequence 7, Appli

Sequence 9, Appli

Sequence 21237, A

Sequence 22, Appli

Sequence 23526, A

RESULT 2  
US-10-087-195-7  
; Sequence 7, Application US/10087195  
; Publication No. US20020193306A1  
; GENERAL INFORMATION:  
; APPLICANT: Nuttall, Patricia, Anne  
; TITLE OF INVENTION: Treatment of Allergic Rhinitis  
; FILE REFERENCE: 2488-1-004  
; CURRENT APPLICATION NUMBER: US/10/087,195  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: PCT/GB00/03287  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 9920673.2  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 7  
; LENGTH: 171  
; TYPE: PRT  
; ORGANISM: FS-HBP 2  
; US-10-087-195-7

Query Match 25.1%; Score 282; DB 13; Length 171;  
Best Local Similarity 37.5%; Pred. No. 1.4e-22;  
Matches 66; Conservative 29; Mismatches 69; Indels 12; Gaps 8;  
Qy 31 PIWAAHLLGKQDQWKSIDQGSVSYVIAKTYENDTGSWSQFKCLOQBIERKE 90  
Db 3 PDWAAEBAANGHAWQDAWKSLSKADVENVYVKAATKNDP-VWGNDFICUVGMANDVNEDEK 61  
Qy 91 TVTSVFTF-ENASPIKYKVNTEKTVAKVFOQYGNIRNAIEQVGGGNNITDTLITFGE 149  
Db 62 SIQASPLFMNNAIDTMQF--ATEKTVAKVQGY-NRENAFRATEDQGVFTDVIAYS-D 117  
Qy 150 LCDVPTVNPAD--QGCEWVKRSKSYKHPDYCPFVENVFCAXDRKQYDINNECY 202  
Db 118 NCDVIVVPGTIDGNEBGEYELWT--TDYDNPANCNLKFNEY-AVGRETDRDVFSACH 170  
RESULT 3  
US-10-085-572-8  
; Sequence 8, Application US/10085572  
; Publication No. US20020151499A1  
; GENERAL INFORMATION:  
; APPLICANT: Paesen, Guido, Christiaan  
; TITLE OF INVENTION: Treatment of Conjunctivitis  
; FILE REFERENCE: 2488-1-003  
; CURRENT APPLICATION NUMBER: US/10/085,572  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB00/03282  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 9920674.0  
; PRIOR FILING DATE: 1999-05-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 8  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: MS-HBP 1  
; US-10-085-572-8

Query Match 22.4%; Score 251.5; DB 13; Length 182;  
Best Local Similarity 35.3%; Pred. No. 3.3e-19;  
Matches 61; Conservative 29; Mismatches 66; Indels 17; Gaps 8;  
Qy 30 NPIWAAHLLGKQDQWKSIDQGSVSYVIAKTYENDTGSWSQFKCLOQ-OBIEKE 87  
Db 1 NPTWAAEALGSKYDQWKSLSKADVENVYVKAATQD-GWGNDFICUVGVTAKIGCK 59  
Qy 88 EDTVTSVFTFNAS-SPIKYKVNTEKTVAKVFOQYGNIRNAIEQVGGGNNIT-DTLI 144  
Db 60 LNATI--LYKRNHLTDLKSHETTIVKAYD--TTENGKQETQGPRTQFEDVFT 112  
Qy 145 FTGELCDVVFPM--NADQG-CELVWKSNSKSYKHPDYCPFVENVFCAKRKT 193  
Db 113 FSDYKNCDVTFVKERSSDEGDIYELWNSEDKIDKIPDCCFTMAYFAQQOKT 165  
RESULT 4  
US-10-087-195-8  
; Sequence 8, Application US/10087195  
; Publication No. US20020193306A1  
; GENERAL INFORMATION:  
; APPLICANT: Nuttall, Patricia, Anne  
; APPLICANT: Paesen, Guido, Christiaan  
; TITLE OF INVENTION: Treatment of Allergic Rhinitis  
; FILE REFERENCE: 2488-1-004  
; CURRENT APPLICATION NUMBER: US/10/087,195  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: PCT/GB00/03287  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 9920673.2  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 8  
; LENGTH: 182  
; TYPE: PRT  
; ORGANISM: MS-HBP 1  
; US-10-087-195-8

Query Match 22.4%; Score 251.5; DB 13; Length 182;  
Best Local Similarity 35.3%; Pred. No. 3.3e-19;  
Matches 61; Conservative 29; Mismatches 66; Indels 17; Gaps 8;  
Qy 30 NPIWAAHLLGKQDQWKSIDQGSVSYVIAKTYENDTGSWSQFKCLOQ-OBIEKE 87  
Db 1 NPTWAAEALGSKYDQWKSLSKADVENVYVKAATQD-GWGNDFICUVGVTAKIGCK 59  
Qy 88 EDTVTSVFTFNAS-SPIKYKVNTEKTVAKVFOQYGNIRNAIEQVGGGNNIT-DTLI 144  
Db 60 LNATI--LYKRNHLTDLKSHETTIVKAYD--TTENGKQETQGPRTQFEDVFT 112  
Qy 145 FTGELCDVVFPM--NADQG-CELVWKSNSKSYKHPDYCPFVENVFCAKRKT 193  
Db 113 FSDYKNCDVTFVKERSSDEGDIYELWNSEDKIDKIPDCCFTMAYFAQQOKT 165  
RESULT 5  
US-10-085-572-6  
; Sequence 6, Application US/10085572  
; Publication No. US20020151499A1  
; GENERAL INFORMATION:  
; APPLICANT: Nuttall, Patricia, Anne  
; APPLICANT: Paesen, Guido, Christiaan  
; TITLE OF INVENTION: Treatment of Conjunctivitis  
; FILE REFERENCE: 2488-1-003  
; CURRENT APPLICATION NUMBER: US/10/085,572  
; CURRENT FILING DATE: 2002-02-27  
; PRIOR APPLICATION NUMBER: PCT/GB00/03282  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: 9920674.0  
; PRIOR FILING DATE: 1999-05-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 6  
; LENGTH: 172  
; TYPE: PRT  
; ORGANISM: FS-HBP 1  
; US-10-085-572-6

Query Match 21.2%; Score 239; DB 13; Length 172;

Best Local Similarity 34.5%; Pred. No. 7.2e-18; Mismatches 82; Indels 10; Gaps 7; Matches 61; Conservative 24; Mismatches 82; Indels 10; Gaps 7; Current Filing Date: 2001-03-21; Prior Application Number: 60/191,078

QY 29 ENPLWHAELLLGKYQDWSKSIDQGVSVYVIAKTYTENDGWSQFKLQVQBIEREE 88 ; Prior Filing Date: 2000-03-21

Db 1 DKPVWADEAANGEHQDWAHKHQLQKLVENYDILKATYKNDP-VWGNDFTCVGAQNLINED 59 ; Prior Application Number: 60/206,848

QY 89 DYTTSFPTFRVASSPKVXNTETKAVFGYKIRNAIEYQGGNITIDTLIFTDG 148 ; Prior Filing Date: 2000-05-23

Db 60 EKVAEWFMMNADTV-YQHTEKAATPDKGY-NKENALTYQEDGQVLTDVLAFSD- 116 ; Prior Application Number: 60/242,578

QY 149 ELCDVDFYVPNAD--QGCELWTKSKYKHWEDYCFFENIFCAKDRKTYDNEECV 202 ; Prior Filing Date: 2000-10-23

Db 117 DNYCYVIALGPGDCSGAGYELWA--TDXTDVASCLEKFENYAA-GLPVRDVYSDCL 170 ; Prior Application Number: 60/253,625

RESULT 6 US-10-087-195-6

; Sequence 6, Application US/10087195

; Publication No. US20020193306A1

; GENERAL INFORMATION:

; APPLICANT: Paesens, Guido, Christian

; TITLE OF INVENTION: Treatment of Allergic Rhinitis

; FILE REFERENCE: 2488-1-004

; CURRENT FILING DATE: US/10/087,195

; CURRENT FILING DATE: 2002-03-01

; PRIOR APPLICATION NUMBER: PCT/GB00/03287

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: 9920673.2

; PRIOR FILING DATE: 1999-09-01

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO: 6

; LENGTH: 172

; TYPE: PRT

; ORGANISM: FS-HBPI

; US-10-087-195-6

Query Match Best Local Similarity 34.5%; Pred. No. 7.2e-18; Length 172; Matches 61; Conservative 24; Mismatches 82; Indels 10; Gaps 7; Current Filing Date: 2001-02-16; Prior Application Number: 60/269,308

QY 29 ENPLWHAELLLGKYQDWSKSIDQGVSVYVIAKTYTENDGWSQFKLQVQBIEREE 88 ; Number of SEQ ID NOS: 14110

Db 1 DKPVWADEAANGEHQDWAHKHQLQKLVENYDILKATYKNDP-VWGNDFTCVGAQNLINED 59 ; Software: FastSEQ For Windows Version 4.0

QY 89 DYTTSFPTFRVASSPKVXNTETKAVFGYKIRNAIEYQGGNITIDTLIFTDG 148 ; SEQ ID NO: 10796

Db 60 EKVAEWFMMNADTV-YQHTEKAATPDKGY-NKENALTYQEDGQVLTDVLAFSD- 116 ; SEQ ID NO: 10796

QY 149 ELCDVDFYVPNAD--QGCELWTKSKYKHWEDYCFFENIFCAKDRKTYDNEECV 202 ; LENGTH: 722

Db 117 DNYCYVIALGPGDCSGAGYELWA--TDXTDVASCLEKFENYAA-GLPVRDVYSDCL 170 ; TYPE: PRT

QY 16 LATQMTSA---KAGENPLWAELLLGKYQDWSKSIDQGVSVYVIAKTYTENDGWSQFKLQVQBIEREE 64 ; ORGANISM: Enterococcus faecalis

Db 204 LVGDKEGTGSSYGPAYKGQNP---ELIKKENGALKQKUDNG---TIDKILNNLYATGD 255 ; US-09-815-242-10796

QY 65 ENDTGSWSQFKLQVQBIERKEEDYTVSFFERNASSPIKTYNV-----TETVKA 116 ;

Db 256 ETNTODAGEBK---KTPPKRKYVIASDST---APPFQNAQDQYVGDVJVR 306 ;

QY 117 V-----FQY-GYKRNIRALTY-QVGG--GUNIITDLIFTDGELCDVFTVNPADQ 162 ;

Db 307 AAELOGRTVERPKIGFSSAVAOAVSGQADGMVAGTID---DRKCAFDFSVPYFDSG 361 ;

QY 163 CELWVKSH---YKPVDFYCFVFNV-----FCAKRTYD 195 ;

Db 362 IQIAVEKGNDIKSYDLKSKVKGKIGESADFLLEKKKYPD 404 ;

RESULT 8 US-09-728-914-4

QY 89 DYTTSFPTFRVASSPKVXNTETKAVFGYKIRNAIEYQGGNITIDTLIFTDG 148 ; Sequence 4, Application US/09728914

Db 60 EKVAEWFMMNADTV-YQHTEKAATPDKGY-NKENALTYQEDGQVLTDVLAFSD- 116 ; Patent No. US20010046499A1

QY 149 ELCDVDFYVPNAD--QGCELWTKSKYKHWEDYCFFENIFCAKDRKTYDNEECV 202 ; General Information:

Db 117 DNYCYVIALGPGDCSGAGYELWA--TDXTDVASCLEKFENYAA-GLPVRDVYSDCL 170 ; APPLICANT: KANTOR, FRED S.

QY 16 LATQMTSA---KAGENPLWAELLLGKYQDWSKSIDQGVSVYVIAKTYTENDGWSQFKLQVQBIEREE 64 ; APPLICANT: FIRKIG, EROL

Db 204 LVGDKEGTGSSYGPAYKGQNP---ELIKKENGALKQKUDNG---TIDKILNNLYATGD 255 ; APPLICANT: DAS, SUBRATA

QY 65 ENDTGSWSQFKLQVQBIERKEEDYTVSFFERNASSPIKTYNV-----TETVKA 116 ; APPLICANT: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING

Db 256 ETNTODAGEBK---KTPPKRKYVIASDST---APPFQNAQDQYVGDVJVR 306 ; TIME OF INVENTION: THEM

QY 117 V-----FQY-GYKRNIRALTY-QVGG--GUNIITDLIFTDGELCDVFTVNPADQ 162 ; CURRENT APPLICATION NUMBER: US/09/728,914

Db 307 AAELOGRTVERPKIGFSSAVAOAVSGQADGMVAGTID---DRKCAFDFSVPYFDSG 361 ; CURRENT FILING DATE: 2000-12-01

QY 163 CELWVKSH---YKPVDFYCFVFNV-----FCAKRTYD 195 ; Prior Application Number: 60/169,048

Db 362 IQIAVEKGNDIKSYDLKSKVKGKIGESADFLLEKKKYPD 404 ; Prior Filing Date: 1999-12-03

QY 89 DYTTSFPTFRVASSPKVXNTETKAVFGYKIRNAIEYQGGNITIDTLIFTDG 148 ; Prior Application Number: 60/240,716

Db 60 EKVAEWFMMNADTV-YQHTEKAATPDKGY-NKENALTYQEDGQVLTDVLAFSD- 116 ; Prior Filing Date: 2000-10-16

QY 149 ELCDVDFYVPNAD--QGCELWTKSKYKHWEDYCFFENIFCAKDRKTYDNEECV 202 ; Number of SEQ ID NOS: 39

Db 117 DNYCYVIALGPGDCSGAGYELWA--TDXTDVASCLEKFENYAA-GLPVRDVYSDCL 170 ; Software: PatentIn Ver. 2.1

QY 16 LATQMTSA---KAGENPLWAELLLGKYQDWSKSIDQGVSVYVIAKTYTENDGWSQFKLQVQBIEREE 64 ; SEQ ID NO: 4

Db 204 LVGDKEGTGSSYGPAYKGQNP---ELIKKENGALKQKUDNG---TIDKILNNLYATGD 255 ; LENGTH: 221

QY 65 ENDTGSWSQFKLQVQBIERKEEDYTVSFFERNASSPIKTYNV-----TETVKA 116 ; TYPE: PRT

Db 256 ETNTODAGEBK---KTPPKRKYVIASDST---APPFQNAQDQYVGDVJVR 306 ; ORGANISM: Ixodes scapularis

QY 117 V-----FQY-GYKRNIRALTY-QVGG--GUNIITDLIFTDGELCDVFTVNPADQ 162 ;

Db 307 AAELOGRTVERPKIGFSSAVAOAVSGQADGMVAGTID---DRKCAFDFSVPYFDSG 361 ;

QY 163 CELWVKSH---YKPVDFYCFVFNV-----FCAKRTYD 195 ;

Db 362 IQIAVEKGNDIKSYDLKSKVKGKIGESADFLLEKKKYPD 404 ;

RESULT 7 US-09-815-242-10796

; Sequence 10796, Application US/09815242

; Patent No. US2002001569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zvorskida, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Cair, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

; FILE REFERENCE: ELTRA.01A

; CURRENT APPLICATION NUMBER: US/09/815,242

Qy 10 TFPVSAALATOET---TSKAGENPWAHEILGK---QDAWKSIDQGSVTVYLA 60 ; SEQ ID NO 2  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 11 WRTYD-VTDFSGNPVGQCNENFMEKER---TPTNYSFORYRSKSN-SWETIDELILKDI 134 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 12 81 WRTYD-VTDFSGNPVGQCNENFMEKER---TPTNYSFORYRSKSN-SWETIDELILKDI 134 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 13 118 FOQYGNIRNAYIEQVQGGLNITDTI-FTGDGLCVFVYPNADOG--CEIWKK-SHY 172 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 14 135 GEHGFPRNMNFRTPIG---IATDNVLVSYWNTVLRIPFTNGERICDLMNNTLS 191 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 15 173 KEPVDPYCTFVNFCARDKRTDIFNHEC 201 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 16 192 QETPDDCLNKFPEYC-NTIQIYRVVYFSC 219 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

RESULT 9  
US-09-728-914-22  
Sequence 22, Application US/09728914  
; Patent No. US2001046499A1  
; GENERAL INFORMATION:  
; APPLICANT: KANTOR, FRED S.  
; APPLICANT: PIKRTG, EROL  
; APPLICANT: DAS, SUBRAYA  
; TITLE OF INVENTION: TICK ANTIGENS AND COMPOSITIONS AND METHODS COMPRISING  
; TITLE OF INVENTION: THEM  
; FILE REFERENCE: YU-107  
; CURRENT APPLICATION NUMBER: US/09/728.914  
; CURRENT FILING DATE: 2000-12-01  
; PRIORITY FILING DATE: 1999-12-03  
; PRIORITY APPLICATION NUMBER: 60/169,048  
; PRIORITY FILING DATE: 2000-10-16  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO: 22  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: *Ixodes scapularis*  
; US-09-728-914-22

Query Match 7.5%; Score 84; DB 9; Length 217;  
Best Local Similarity 24.1%; Pred. No. 0.82; Mismatches 48; Indels 20; Gaps 3;  
Matches 27; Conservative 17; Mismatches 48; Indels 20; Gaps 3;

Qy 17 99 RWAASSPIKQYNTETTAVGQYQYKIRNATEQYQVQGGLNITDTI-FTGDGLCVFVYPNADOG 148 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 18 135 ADPTRLRISRTQVPLRSCLLWVKTEFLNPLRCRELFDFCNMR3DF 186 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Clostridium perfringens*  
; Us-09-932-183A-2

RESULT 10  
US-09-932-183A-2  
Sequence 2, Application US/09932183A  
; Patent No. US2002012764A1  
; GENERAL INFORMATION:  
; APPLICANT: Estell, David A.  
; TITLE OF INVENTION: Proteases from Gram-Positive Organism  
; FILE REFERENCE: G0394C1-US  
; CURRENT APPLICATION NUMBER: US/09/932,183A  
; CURRENT FILING DATE: 2001-08-17  
; PRIORITY APPLICATION NUMBER: US 09/1308,375  
; PRIORITY FILING DATE: 1998-05-14  
; PRIORITY APPLICATION NUMBER: PCT/US98/118828  
; PRIORITY FILING DATE: 1998-09-08  
; PRIORITY APPLICATION NUMBER: EP9719636.4  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSEQ for Windows Version 3.0

Query Match 7.3%; Score 82; DB 15; Length 381;  
Best Local Similarity 21.8%; Pred. No. 3; Mismatches 56; Indels 28; Gaps 3;  
Matches 29; Conservative 20; Mismatches 56; Indels 28; Gaps 3;

Qy 19 9 LTFVSAALATOETTSKAGENPWAHEILG---KQDAWKSIDQGSVTVYLA 57 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 20 35 LEVDQTKAASAEETINNESEVNEELDADEPMQLQDNDRPNVFLPLKHDIMWYFKAVASFW 94 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 21 58 VLAKKTYENDGQSGQFCLQVOELERKEBDYTVSFTERNASPI---KYYVY 110 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

Qy 22 95 TVEVDQJGMDW---ERKNGDQFISRLAFAASDGVINENIERSNE 144 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-09-932-183A-2

RESULT 11  
US-10-369-493-5686  
; Sequence 5686, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xianteng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIORITY FILING DATE: 2002-02-21  
; PRIORITY FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO: 5686  
; LENGTH: 381  
; TYPE: PRT  
; ORGANISM: *Cloenorhabditis elegans*  
; Us-10-369-493-5686

Query Match 7.3%; Score 82; DB 15; Length 381;  
Best Local Similarity 21.8%; Pred. No. 3; Mismatches 56; Indels 28; Gaps 3;  
Matches 29; Conservative 20; Mismatches 56; Indels 28; Gaps 3;

Qy 23 9 LTFVSAALATOETTSKAGENPWAHEILG---KQDAWKSIDQGSVTVYLA 57 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-10-369-493-5686

Qy 24 35 LEVDQTKAASAEETINNESEVNEELDADEPMQLQDNDRPNVFLPLKHDIMWYFKAVASFW 94 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-10-369-493-5686

Qy 25 58 VLAKKTYENDGQSGQFCLQVOELERKEBDYTVSFTERNASPI---KYYVY 110 ;  
; :  
; LENGTH: 2285  
; TYPE: PRT  
; ORGANISM: *Bacillus subtilis*  
; Us-10-369-493-5686

RESULT 12  
US-10-389-566-2357  
; Sequence 2357, Application US/10389566  
; Publication 2357, Application US/200400225202A1  
; GENERAL INFORMATION:

APPLICANT: Monsanto Technology, LLC  
 APPLICANT: Laurie, Cathy C  
 TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants  
 FILE REFERENCE: 38-77152900D  
 CURRENT APPLICATION NUMBER: US/10/389,566  
 CURRENT FILING DATE: 2003-03-31  
 PRIORITY FILING DATE: 2002-03-15  
 PRIORITY APPLICATION NUMBER: US 60/391,786  
 PRIORITY FILING DATE: 2002-06-25  
 PRIORITY APPLICATION NUMBER: US 60/392,018  
 SEQ ID NO: 2357  
 LENGTH: 627  
 TYPE: PRT  
 ORGANISM: *Rickettsia prowazekii*  
 US-10-389-566-2357

RESULT 14  
 US-10-291-583-83  
 Query Match 7.2%; Score 81.5; DB 16; Length 627;  
 Best Local Similarity 28.2%; Pred. No. 6.7;  
 Matches 33; Conservative 15; Mismatches 42; Indels 27; Gaps 7;  
 SEQ ID NO: 2459  
 LENGTH: 627  
 SOFTWARE: PatentIn version 3.2

APPLICANT: Gao, Guanping  
 APPLICANT: Wilson, James M.  
 APPLICANT: Alvira, Mauricio  
 TITLE OF INVENTION: A Method of Detecting and/or Identifying Adeno-Associated Viral Sequences and Isolating No. US20030138772A1  
 FILE REFERENCE: UPN-027350USA  
 CURRENT APPLICATION NUMBER: US/10/391,583  
 CURRENT FILING DATE: 2002-11-12  
 PRIORITY FILING DATE: 2001-11-13  
 PRIORITY APPLICATION NUMBER: US 60/341,117  
 PRIORITY FILING DATE: 2001-11-17  
 PRIORITY APPLICATION NUMBER: US 60/377,066  
 PRIORITY FILING DATE: 2002-05-01  
 PRIORITY APPLICATION NUMBER: US 60/386,675  
 PRIORITY FILING DATE: 2002-06-05  
 NUMBER OF SEQ ID NOS: 120  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO: 83  
 LENGTH: 738  
 TYPE: PRT  
 ORGANISM: capsid protein of AAV serotype, clone 29.5V1  
 US-10-291-583-83

RESULT 13  
 US-10-090-624-12  
 Sequence 12, Application US/10090624  
 Publication No. US20020132335A1  
 GENERAL INFORMATION:  
 APPLICANT: TAKAKURA, Hikaru  
 APPLICANT: MORIHITA, MiO  
 APPLICANT: SHIMODOU, Tomoko  
 APPLICANT: ASADA, Kiyoko  
 APPLICANT: KATO, Ikuo  
 TITLE OF INVENTION: SYSTEM FOR EXPRESSING HYPERTHERMOSTABLE FILE REFERENCE: TAKAKURA-6  
 CURRENT APPLICATION NUMBER: US/10/090,624  
 CURRENT FILING DATE: 2002-03-05  
 PRIORITY APPLICATION NUMBER: 09/445,472  
 PRIORITY FILING DATE: 1999-12-06  
 PRIORITY APPLICATION NUMBER: 151969/1997  
 PRIORITY FILING DATE: 1997-06-10  
 NUMBER OF SEQ ID NOS: 33  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 12  
 LENGTH: 659  
 TYPE: PRT  
 ORGANISM: *Thermococcus celer*  
 US-10-090-624-12

Query Match 7.2%; Score 80.5; DB 14; Length 738;  
 Best Local Similarity 27.5%; Pred. No. 11; Mismatches 56; Indels 33; Gaps 10;  
 Matches 41; Conservative 19; Mismatches 56; Indels 33; Gaps 10;  
 SEQ ID NO: 120  
 LENGTH: 738  
 SOFTWARE: PatentIn version 3.1

APPLICANT: Gao, Guanping  
 APPLICANT: Wilson, James M.  
 APPLICANT: Alvira, Mauricio  
 TITLE OF INVENTION: A Method of Detecting and/or Identifying Adeno-Associated Viral Sequences and Isolating No. US20030138772A1  
 FILE REFERENCE: UPN-027350USA  
 CURRENT APPLICATION NUMBER: US/10/391,583  
 CURRENT FILING DATE: 2002-11-12  
 PRIORITY APPLICATION NUMBER: US 60/356,607  
 PRIORITY FILING DATE: 2001-11-13  
 PRIORITY APPLICATION NUMBER: US 60/341,117  
 PRIORITY FILING DATE: 2001-12-17  
 PRIORITY APPLICATION NUMBER: US 60/377,066  
 PRIORITY FILING DATE: 2002-05-01  
 PRIORITY APPLICATION NUMBER: US 60/386,675  
 PRIORITY FILING DATE: 2002-06-05  
 PRIORITY APPLICATION NUMBER: US 60/387,067

; PRIOR FILING DATE: 2002-06-05  
; NUMBER OF SEQ ID NOS: 120  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 92  
; LENGTH: 738  
; TYPE: PRT  
; ORGANISM: capsid protein of AAV serotype, clone 43.1  
; US-10-291-533-92  
  
Query Match 7.1%; Score 79.5; DB 14; Length 738;  
Best Local Similarity 28.3%; Pred. No. 14; Mismatches 60; Indels 35; Gaps 12;  
Matches 45; Conservative 19; Mismatches 60; Indels 35; Gaps 12;  
  
QY 13 SAAIAQAEETSAKAGENPLWAHEELIGKQD-ANWSIDOGVSTIVLAKTIWENDTOSW 71  
Db 233 STWLGDRVITTSRTRT----WA---LPTVNNHLYKQISNGTSGGST-NDNTVPGYSPW 282  
QY 72 G---SQTCKLQVQEIERKEEDYTVTSVFTRNASSPIKYVNTETVRAVFO YGYKIR 126  
Db 283 GYFDPNRTHC---HFSPPRMDWRLINNNGRPRKQNLKFLNT -QVKETVQMEGKTKIA 336  
QY 127 NAYEYQVGGGLNITDTL-IFTDGECLCDVFPYV-NAQGC 163  
Db 337 N-----NLSTTIVQVFTDSEY-QLPVVPGSAHQGC 364

Search completed: March 9, 2004, 13:36:50  
Job time : 34 secs

GenCore version 5.1.6  
(c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using SW model

Run on:

March 9, 2004, 13:30:31 ; (Search time 20 seconds)

1005.201 Million cell updates/sec

Title: US-09-555-296B-4

Sequence: I KRMQVVLILITFVVSALATQA. .... DRKYDIFNSECVYNGEPWL 209

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR:78:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	96.5	8.6	621	F97862
2	96	8.5	650	G701258
3	87	7.7	639	B49132
4	86	7.6	2747	85
5	85	7.6	656	A87112
6	84	7.5	621	H71645
7	84.5	7.5	917	AF1394
8	83	7.4	2285	T12796
9	82.5	7.3	318	C69192
10	82	7.3	163	C97308
11	82	7.3	360	T17996
12	82	7.3	381	T1886
13	82	7.3	390	D82922
14	82	7.3	637	T08530
15	82	7.3	2	S22992
16	81.5	7.2	627	D71729
17	80.5	7.2	621	A71961
18	79.5	7.1	621	864546
19	79.5	7.1	725	AG2547
20	78.5	7.0	455	A75121
21	78.5	7.0	864	S60441
22	78	6.9	215	S26669
23	78	6.9	523	O4CKA3
24	78	6.9	1871	S27938
25	77.5	6.9	223	T12076
26	77.5	6.9	506	T25870
27	77	6.8	241	T26909
28	77	6.8	331	D81409
29	77	6.8	780	H84453

## ALIGNMENTS

RESULT	1
Query	F97862
Match	heat shock protein httpG [imported] - Rickettsia conorii (strain Malish 7)
Best Local Similarity	8.6%
Score	96.5
DB	2
ID	Length 621;
Matches	43;
Conservative	21.0%;
Pred.	Pred. No. 1;2;
Mismatches	46;
Indels	81;
Gaps	35;
Length	35;
Description	heat shock protein
1	heat shock protein
2	probable heat shock protein
3	probable heat shock protein
4	probable heat shock protein
5	probable heat shock protein
6	probable heat shock protein
7	probable transglyc
8	probable transglyc
9	probable actyltra
10	probable actyltra
11	probable actyltra
12	probable actyltra
13	conserved hypothetical protein
14	conserved hypothetical protein
15	conserved hypothetical protein
16	conserved hypothetical protein
17	conserved hypothetical protein
18	conserved hypothetical protein
19	conserved hypothetical protein
20	hypothetical protein
21	hypothetical protein
22	hypothetical protein
23	hypothetical protein
24	hypothetical protein
25	hypothetical protein
26	hypothetical protein
27	hypothetical protein
28	hypothetical protein
29	hypothetical protein

transferrin-bindin  
poly-beta-hydroxyb  
probable RNA helic  
hypothetical prote  
conserved hypothet  
deoxyribonucleic kina  
hypothetical prote  
lipase-like protei  
hypothetical prote  
probable arylsulfa  
heat-shock protei  
probable Ctpase  
hypothetical prote  
hypothetical prote  
probable transmemb

C;Species: Rickettsia conorii  
C;Accession: F97862  
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barber, V.; Samson, D.  
Science, 293, 2093-2098, 2001  
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.  
A;Reference number: A97700; MUID:21442074; PMID:1157893  
A;Accession: F97862  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-621 <KUR>  
A;Cross-references: GB:AE005914; PIDN:AA03840.1; PID:915620441; GSPDB:GN00173  
C;Genes: httpG  
C;Superfamily: heat shock protein 90

Query Match 8.6%; Score 96.5; DB 2; Length 621;  
Best Local Similarity 21.0%; Pred. No. 1;2;  
Matches 43; Conservative 21.0%; Mismatches 81; Indels 35; Gaps 10;

QY 11 FV3SALLATORETTAKAGENP-LWAHELLGKYY-ODAWKSIDQSYVSYVTLAKTYYEN 66  
Db 127 YSSFMWADKVTVTRKAGEDKVW-ESDGIGEYTVSDSKDREFTGRGTVBILHKK--EE 182

QY 67 DTGSNSGSQFKCLOQYQBIERKEBETYVSVPTF-----RNASSPIKYNTETKAV 117  
Db 183 DT----FLDHF---LKHIVKSYSDHIAVPIYFDEAGNNBQIQLNSASALWTRPSETEEQ 237

QY 118 PQYGMKRNIAE-----YQUGGGLNITDFTLFTGELCVYVYNAQOCELMVK- 169  
Db 238 YKEPYKSLSYAIDDPWITMENKNGEATFPTNLIFPSKTFDLFH-PDKRKRVYIKRV 296

QY 170 ---SHYKAVPDYKTFVFRVFCQD 190  
Db 297 FISDNTDILPSYRFLRGRVQD 321

RESULT 2

heat shock protein 90 (httpG) homolog - Lyme disease spirochete  
N;Alternate names: C62.5 heat shock protein  
C;Species: Borrelia burgdorferi (lyme disease spirochete)  
C;Date: 13-Feb-1998 #Sequence\_revision 13-Feb-1998 #Text\_change 20-Aug-1999  
C;Accession: G70169; I40247  
R;Fraser, C.M.; Cajjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; Wilson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.; Nature 390, 580-586, 1997  
A;Authors: Smith, H.O.; Venter, J.C.



RESULT 7  
AF1394  
autolysin, amidase [imported] - *Listeria monocytogenes* (strain EGD-e)



A;Status: preliminary; translated from GB/EMBL/DDBT  
 A;Molecule type: DNA  
 A;Residues: 1-381 <WIL>  
 A;Cross-references: EMBL:235637; PIDN:CAA84688.1; GSPDB:GN00021; CESP:C03C10\_3  
 A;Experimental source: clone C03C10  
 C;Genetics:  
 A;Gene: CESP:C03C10\_3  
 A;Map position: 3  
 A;Intron: 18/3; 13/7/3; 25/2  
 C;Superfamily: ribonucleoside reductase small subunit

Query Match 7.3%; Score 82; DB 2; Length 381;  
 Best Local Similarity 21.8%; Pred. No. 13; Mismatches 56; Indels 28; Gaps 3;  
 Matches 29; Conservative 20; Mismatches 56; Indels 28; Gaps 3;  
 保守型 9 LTFVSAALATQAETTSKAKGENPLWMAHEELGKQDAWKSIDQGSVTVI-VLAKTTEN 66  
 Db 35 LEIVDQTKASABETTNESEVNEFLDAEPMQLDQDRFVFLPKHDINWYKQKAVW 94  
 QY 58 VLAKTTENDTGSGWSQFKLQVQEBERKEEDYTVTSVFTRNASSPL-----KYNW 110  
 95 TVERBDLGKDMNDW-----ERKNGDEQFISRILAFFAASDDGIVNENLCERFSNE 144  
 QY 111 TETVTKAVFOGYK 123  
 Db 145 VQVSEARFFYQFQ 157

RESULT 13

conserved hypothetical UU198 [imported] - Ureaplasma urealyticum

QY: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C;Accession: D82922  
 R;Glass, J.I., Lefkowitz, E.J.; Glass, J.S.; Heinrich, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to Genbank, February 2000

A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir

A;Reference number: A82870

A;Accession: D82222

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-390 &lt;GLA&gt;

A;Cross-references: GB:AE002119; GB:AF222894; NID:96899153; PIDN:AAF30605.1; GSPDB:GN001

A;Experimental source: serovar 3; biovar 1

C;Genetics:

A;Gene: UU198

A;Genetic code: SGCC3

Query Match 7.3%; Score 82; DB 2; Length 390;  
 Best Local Similarity 22.3%; Pred. No. 13; Mismatches 51; Indels 22; Gaps 5;  
 Matches 29; Conservative 28; Mismatches 51; Indels 22; Gaps 5;

保守型

8 LTFVSAALATQAETTSKAKGENPLWMAHEELGKQDAWKSIDQGSVTVI-VLAKTTEN 66  
 Db 167 ILLVSTGQGANASGTAASPLKSKERKPKHDINWYKQKAVW 94  
 QY 67 DTQWSGSPKCLQVQEBERKEEDYTVTSVFTRNASSPL-----KYNW 110  
 224 NTQAW-----TNISKDNVGDGSIYL-----STGFLKKNYDQIAKGKYLQNK 268  
 QY 124 NTRMATEQV 133  
 Db 269 DLKMLPFB1 278

RESULT 14

trg protein - Enterobacter aerogenes plasmid R751

C;Species: Enterobacter aerogenes

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C;Accession: T08330  
 R;Thorsred, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.  
 Plasmid 36, 95-111, 1996

A;Title: Conservation of the genetic switch between replication and transfer genes c  
 A;Reference number: 216434; MUID:97113926; PMID:8954881  
 A;Accession: T08330  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-677 <THO>  
 A;Cross-references: EMBL:U67194; NID:91572520; PIDN: AAC64474.1; PID:91572579  
 C;Genetics:  
 A;Gene: trg  
 A;Genome: Plasmid R751

Query Match 7.3%; Score 82; DB 2; Length 637;  
 Best Local Similarity 18.3%; Pred. No. 25; Mismatches 89; Indels 86; Gaps 7;  
 Matches 46; Conservative 30; Mismatches 89; Indels 86; Gaps 7;  
 保守型 5 VLLTFVSAALATQAETTSKAKGENPLWMAHEELGKQDAWKSIDQGSVTVI-VLAKTTEN 66  
 Db 90 ILLVSTGQGANASGTAASPLKSKERKPKHDINWYKQKAVW 94  
 QY 38 --LLGKQDAWKSID-----QGSVTVI-VLAKTTENDTG-----SWQSQFKLQV 80  
 Db 150 PTATGTVVGGQDQKONFVFLRHSQPERHVTATRSGKGVLVUPTILWGSASVITDL 209

Query Match 7.3%; Score 82; DB 2; Length 637;  
 Best Local Similarity 18.3%; Pred. No. 25; Mismatches 89; Indels 86; Gaps 7;  
 Matches 46; Conservative 30; Mismatches 89; Indels 86; Gaps 7;  
 保守型 5 VLLTFVSAALATQAETTSKAKGENPLWMAHEELGKQDAWKSIDQGSVTVI-VLAKTTEN 66  
 Db 90 ILLVSTGQGANASGTAASPLKSKERKPKHDINWYKQKAVW 94  
 QY 38 --LLGKQDAWKSID-----QGSVTVI-VLAKTTENDTG-----SWQSQFKLQV 80  
 Db 150 PTATGTVVGGQDQKONFVFLRHSQPERHVTATRSGKGVLVUPTILWGSASVITDL 209

R;Lanka, E.  
 submitted to the EMBL Data Library, August 1990  
 A;Reference number: S42274  
 A;Accession: S42274  
 A;Molecule type: DNA  
 A;Residues: 1-228; D'; 630-637 <LAN>

A;Cross-references: EMBL:X54458; NID:942656; PIDN:CAA38327.1; PID:942657  
 A;Gene: trg  
 A;Genome: plasmid

Query Match 7.3%; Score 82; DB 2; Length 637;  
 Best Local Similarity 18.3%; Pred. No. 25; Mismatches 89; Indels 86; Gaps 7;  
 Matches 46; Conservative 30; Mismatches 89; Indels 86; Gaps 7;

QY 5 VLLTFVSAALATQAETTSKAKGENPLWMAHEELGKQDAWKSIDQGSVTVI-VLAKTTEN 66  
 Db 90 ILLVSTGQGANASGTAASPLKSKERKPKHDINWYKQKAVW 94  
 QY 38 --LLGKQDAWKSID-----QGSVTVI-VLAKTTENDTG-----SWQSQFKLQV 80  
 Db 150 PTATGTVVGGQDQKONFVFLRHSQPERHVTATRSGKGVLVUPTILWGSASVITDL 209

QY 81 QBIERKEEYNTVSFERNASSPIKYNTIEVKANVQYQGNIRAIETQVGGGLNT 140  
 Db 210 ----KGELWALTAGWRQKHAKNQVLRFBPASTSGGVWNPLIDEIRGTEYEVGDYNA 264  
 QY 141 DTLLFTDGLLCDVYV-----PNADQGCE 164  
 Db 265 TLIVDPDGKGDLSDWQKTAFAALLVGVILHALYKAKDDGGTATLPSVDAMLADPNRDIG-E 323  
 QY 165 LMVKKSHYKV 175  
 Db 324 LMWMEMATYGHV 334

Search completed: March 9, 2004, 13:34:01  
Job time : 22 secs

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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Run on: March 9, 2004, 13:30:56 ; Search time 17 seconds (without alignments) 640.157 Million cell updates/sec																																																																																																																																																																																																																																																																																																																																																																																																																																																									
Perfect score: 1125	US-09-555-296B-4	Sequence: 1 MRMQVLLTFVSLATOA.....DRKTYDIFNEBCVYNGEPML 209	Scoring table: BLOSUM62	Gapop 10.0 , Gapext: 0.5	Searched: 141681 seqs, 52070155 residues	Total number of hits satisfying chosen parameters: 141681	Minimum DB seq length: 0	Maximum DB seq length: 200000000	Post-processing: Minimum Match 0%, Maximum Match 100%, Listing first 45 summaries																																																																																																																																																																																																																																																																																																																																																																																																																																																
Database : SwissProt_42;*																																																																																																																																																																																																																																																																																																																																																																																																																																																									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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<table border="1" style="width: 100%; border-collapse: collapse;"> <thead> <tr> <th style="text-align: left; padding: 2px;">Result No.</th> <th style="text-align: left; padding: 2px;">Score</th> <th style="text-align: left; padding: 2px;">Query Match Length</th> <th style="text-align: left; padding: 2px;">DB ID</th> <th style="text-align: left; padding: 2px;">Description</th> </tr> </thead> <tbody> <tr> <td style="padding: 2px;">1</td><td style="padding: 2px;">290.5</td><td style="padding: 2px;">25.8</td><td style="padding: 2px;">190</td><td style="padding: 2px;">1 HBP2_RHIAPI</td></tr> <tr> <td style="padding: 2px;">2</td><td style="padding: 2px;">265</td><td style="padding: 2px;">23.6</td><td style="padding: 2px;">200</td><td style="padding: 2px;">1 HBP2_RHIAPI</td></tr> <tr> <td style="padding: 2px;">3</td><td style="padding: 2px;">252</td><td style="padding: 2px;">22.4</td><td style="padding: 2px;">190</td><td style="padding: 2px;">1 HBP2_RHIAPI</td></tr> <tr> <td style="padding: 2px;">4</td><td style="padding: 2px;">97.5</td><td style="padding: 2px;">8.7</td><td style="padding: 2px;">174</td><td style="padding: 2px;">1 HBP2_RHIAPI</td></tr> <tr> <td style="padding: 2px;">5</td><td style="padding: 2px;">96.5</td><td style="padding: 2px;">8.6</td><td style="padding: 2px;">162</td><td style="padding: 2px;">1 HPG_RICCN</td></tr> <tr> <td style="padding: 2px;">6</td><td style="padding: 2px;">96</td><td style="padding: 2px;">8.5</td><td style="padding: 2px;">615</td><td style="padding: 2px;">1 HPG_BORBU</td></tr> <tr> <td style="padding: 2px;">7</td><td style="padding: 2px;">87</td><td style="padding: 2px;">7.7</td><td style="padding: 2px;">639</td><td style="padding: 2px;">1 HPG_TERPA</td></tr> <tr> <td style="padding: 2px;">8</td><td style="padding: 2px;">86</td><td style="padding: 2px;">7.6</td><td style="padding: 2px;">2778</td><td style="padding: 2px;">1 FAF_DROME</td></tr> <tr> <td style="padding: 2px;">9</td><td style="padding: 2px;">85</td><td style="padding: 2px;">7.6</td><td style="padding: 2px;">656</td><td style="padding: 2px;">1 HPG_NUCLE</td></tr> <tr> <td style="padding: 2px;">10</td><td style="padding: 2px;">84.5</td><td style="padding: 2px;">7.5</td><td style="padding: 2px;">621</td><td style="padding: 2px;">1 HPG_RICPR</td></tr> <tr> <td style="padding: 2px;">11</td><td style="padding: 2px;">82.5</td><td style="padding: 2px;">7.3</td><td style="padding: 2px;">318</td><td style="padding: 2px;">1 YEG92_METHR</td></tr> <tr> <td style="padding: 2px;">12</td><td style="padding: 2px;">82</td><td style="padding: 2px;">7.3</td><td style="padding: 2px;">381</td><td style="padding: 2px;">1 RTR2_CABEF</td></tr> <tr> <td style="padding: 2px;">13</td><td style="padding: 2px;">82</td><td style="padding: 2px;">7.3</td><td style="padding: 2px;">637</td><td style="padding: 2px;">1 TROS_ECOLI</td></tr> <tr> <td style="padding: 2px;">14</td><td style="padding: 2px;">81.5</td><td style="padding: 2px;">7.2</td><td style="padding: 2px;">627</td><td style="padding: 2px;">1 DNAK_RICPR</td></tr> <tr> <td style="padding: 2px;">15</td><td style="padding: 2px;">81</td><td style="padding: 2px;">7.2</td><td style="padding: 2px;">700</td><td style="padding: 2px;">1 HSPC_DTC01</td></tr> <tr> <td style="padding: 2px;">16</td><td style="padding: 2px;">80.5</td><td style="padding: 2px;">7.2</td><td style="padding: 2px;">621</td><td style="padding: 2px;">1 HPG_HELPD</td></tr> <tr> <td style="padding: 2px;">17</td><td style="padding: 2px;">79.5</td><td style="padding: 2px;">7.1</td><td style="padding: 2px;">629</td><td style="padding: 2px;">1 HPG_HELPD</td></tr> <tr> <td style="padding: 2px;">18</td><td style="padding: 2px;">79.5</td><td style="padding: 2px;">7.1</td><td style="padding: 2px;">629</td><td style="padding: 2px;">1 HPG_CHUTE</td></tr> <tr> <td style="padding: 2px;">19</td><td style="padding: 2px;">78.5</td><td style="padding: 2px;">7.1</td><td style="padding: 2px;">725</td><td style="padding: 2px;">1 FTKL_ANASP</td></tr> <tr> <td style="padding: 2px;">20</td><td style="padding: 2px;">78.0</td><td style="padding: 2px;">7.0</td><td style="padding: 2px;">864</td><td style="padding: 2px;">1 YEG3M_YEST</td></tr> <tr> <td style="padding: 2px;">21</td><td style="padding: 2px;">78</td><td style="padding: 2px;">6.9</td><td style="padding: 2px;">215</td><td style="padding: 2px;">1 NO22_SOBYN</td></tr> <tr> <td style="padding: 2px;">22</td><td style="padding: 2px;">77</td><td style="padding: 2px;">6.8</td><td style="padding: 2px;">523</td><td style="padding: 2px;">1 C5C_CAMMA</td></tr> <tr> <td style="padding: 2px;">23</td><td style="padding: 2px;">77</td><td style="padding: 2px;">6.8</td><td style="padding: 2px;">909</td><td style="padding: 2px;">1 HBX_ADMINI</td></tr> <tr> <td style="padding: 2px;">24</td><td style="padding: 2px;">76.5</td><td style="padding: 2px;">6.8</td><td style="padding: 2px;">393</td><td style="padding: 2px;">1 IDH_STRTO</td></tr> <tr> <td style="padding: 2px;">25</td><td style="padding: 2px;">76.5</td><td style="padding: 2px;">6.8</td><td style="padding: 2px;">724</td><td style="padding: 2px;">1 DDX4_HUMAN</td></tr> <tr> <td style="padding: 2px;">26</td><td style="padding: 2px;">76</td><td style="padding: 2px;">6.8</td><td style="padding: 2px;">260</td><td style="padding: 2px;">1 DCK_MOUSE</td></tr> <tr> <td style="padding: 2px;">27</td><td style="padding: 2px;">76</td><td style="padding: 2px;">6.8</td><td style="padding: 2px;">1031</td><td style="padding: 2px;">1 YDQ9_SCBPO</td></tr> <tr> <td style="padding: 2px;">28</td><td style="padding: 2px;">76</td><td style="padding: 2px;">6.8</td><td style="padding: 2px;">1066</td><td style="padding: 2px;">1 HYSA_STPRN</td></tr> <tr> <td style="padding: 2px;">29</td><td style="padding: 2px;">76</td><td style="padding: 2px;">6.8</td><td style="padding: 2px;">1068</td><td style="padding: 2px;">1 TR1_SULG</td></tr> <tr> <td style="padding: 2px;">30</td><td style="padding: 2px;">75</td><td style="padding: 2px;">6.7</td><td style="padding: 2px;">1489</td><td style="padding: 2px;">1 RQG2_SCBPO</td></tr> <tr> <td style="padding: 2px;">31</td><td style="padding: 2px;">75</td><td style="padding: 2px;">6.7</td><td style="padding: 2px;">414</td><td style="padding: 2px;">1 Y078_MEJVA</td></tr> <tr> <td style="padding: 2px;">32</td><td style="padding: 2px;">6.7</td><td style="padding: 2px;">424</td><td style="padding: 2px;">1 PORA_CAME</td><td></td></tr> <tr> <td style="padding: 2px;">33</td><td style="padding: 2px;">75</td><td style="padding: 2px;">6.7</td><td style="padding: 2px;">566</td><td style="padding: 2px;">1 BCDO_RAT</td></tr> </tbody> </table>										Result No.	Score	Query Match Length	DB ID	Description	1	290.5	25.8	190	1 HBP2_RHIAPI	2	265	23.6	200	1 HBP2_RHIAPI	3	252	22.4	190	1 HBP2_RHIAPI	4	97.5	8.7	174	1 HBP2_RHIAPI	5	96.5	8.6	162	1 HPG_RICCN	6	96	8.5	615	1 HPG_BORBU	7	87	7.7	639	1 HPG_TERPA	8	86	7.6	2778	1 FAF_DROME	9	85	7.6	656	1 HPG_NUCLE	10	84.5	7.5	621	1 HPG_RICPR	11	82.5	7.3	318	1 YEG92_METHR	12	82	7.3	381	1 RTR2_CABEF	13	82	7.3	637	1 TROS_ECOLI	14	81.5	7.2	627	1 DNAK_RICPR	15	81	7.2	700	1 HSPC_DTC01	16	80.5	7.2	621	1 HPG_HELPD	17	79.5	7.1	629	1 HPG_HELPD	18	79.5	7.1	629	1 HPG_CHUTE	19	78.5	7.1	725	1 FTKL_ANASP	20	78.0	7.0	864	1 YEG3M_YEST	21	78	6.9	215	1 NO22_SOBYN	22	77	6.8	523	1 C5C_CAMMA	23	77	6.8	909	1 HBX_ADMINI	24	76.5	6.8	393	1 IDH_STRTO	25	76.5	6.8	724	1 DDX4_HUMAN	26	76	6.8	260	1 DCK_MOUSE	27	76	6.8	1031	1 YDQ9_SCBPO	28	76	6.8	1066	1 HYSA_STPRN	29	76	6.8	1068	1 TR1_SULG	30	75	6.7	1489	1 RQG2_SCBPO	31	75	6.7	414	1 Y078_MEJVA	32	6.7	424	1 PORA_CAME		33	75	6.7	566	1 BCDO_RAT																																																																																																																																																																																																																																																																						
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Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_licensing@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_licensing@isb-sib.ch</a>).</td></tr> <tr> <td style="padding: 2px;">CC</td><td style="padding: 2px;">DR</td><td style="padding: 2px;">EMBL; U96081; AAC6107.1; -.</td><td style="padding: 2px;">DR</td><td style="padding: 2px;">EMBL; U96081; AAC6107.1; -.</td><td style="padding: 2px;">CC</td><td style="padding: 2px;">DR</td><td style="padding: 2px;">EMBL; U96081; AAC6107.1; -.</td><td style="padding: 2px;">CC</td><td style="padding: 2px;">DR</td></tr> <tr> <td style="padding: 2px;">CC</td><td style="padding: 2px;">DR</td><td style="padding: 2px;">PDB; 1QFT; 1QFT-00.</td><td style="padding: 2px;">DR</td><td style="padding: 2px;">PDB; 1QFT; 1QFT-00.</td><td style="padding: 2px;">CC</td><td style="padding: 2px;">DR</td><td style="padding: 2px;">PDB; 1QFT; 1QFT-00.</td><td style="padding: 2px;">CC</td><td style="padding: 2px;">DR</td></tr> <tr> <td style="padding: 2px;">CC</td><td style="padding: 2px;">DR</td><td style="padding: 2px;">InterPro; 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ID	077421_RHIAPI	077421_RHIAPI	AC	077421;	-	DT	30-MAY-2000	30-MAY-2000	DT	(Rel. 39, Created)	-	DT	28-FEB-2003	30-MAY-2000	DT	(Rel. 39, Last annotation update)	-	DB	Rhipicephalus-specific histamine-binding protein 2 precursor (FS-HBP2).	Rhipicephalus-specific histamine-binding protein 2 precursor (FS-HBP2).	DB	Rhipicephalus-specific histamine-binding protein 2 precursor (FS-HBP2).	DB	RA	Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.	Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.	RA	Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari; Parasitiformes; Ixodida; Ixodidae; Rhipicephalus.	RA	RX	[1]	SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS).	RX	SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS).	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CC	-1- FUNCTION: Binds histamine with a high-affinity. The ability to outcompete histamine receptors indicates that its function is to suppress inflammation around blood feeding.	CC	CC	SUBCELLULAR LOCATION: Secreted.	SUBCELLULAR LOCATION: Secreted.	CC	SUBCELLULAR LOCATION: Secreted.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_licensing@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_licensing@isb-sib.ch</a> ).										CC	DR	EMBL; U96081; AAC6107.1; -.	DR	EMBL; U96081; AAC6107.1; -.	CC	DR	EMBL; U96081; AAC6107.1; -.	CC	DR	CC	DR	PDB; 1QFT; 1QFT-00.	DR	PDB; 1QFT; 1QFT-00.	CC	DR	PDB; 1QFT; 1QFT-00.	CC	DR	CC	DR	InterPro; IPR02970; His binding.	DR	InterPro; IPR02970; His binding.	CC	DR	InterPro; IPR02970; His binding.	CC	DR	CC	DR	ProDom; P01298; His binding; 1.	DR	ProDom; P01298; His binding; 1.	CC	DR	ProDom; P01298; His binding; 1.	CC	DR	CC	FT	FTD; P01295; His binding; 1.	FT	FTD; P01295; His binding; 1.	CC	FT	FTD; P01295; His binding; 1.	CC	FT	CC	FT	FTD; P01295; His binding; 1.	FT	FTD; P01295; His binding; 1.	CC	FT	FTD; P01295; His binding; 1.	CC	FT	CC	FT	FTD; P01295; His binding; 1.	FT	FTD; P01295; His binding; 1.	CC	FT	FTD; P01295; His binding; 1.	CC	FT	CC	FT	FTD; P01295; His binding; 1.	FT	FTD; P01295; His binding; 1.	CC	FT	FTD; P01295; His binding; 1.	CC	FT	CC	FT	FTD; P01295; His binding; 1.	FT	FTD; P01295; His binding; 1.	CC	FT	FTD; P01295; His binding; 1.	CC	FT	CC	FT	FTD; P01295; His binding; 1.	FT	FTD; P01295; His binding; 1.	CC	FT	FTD; P01295; His binding; 1.	CC	FT	CC	FT	FTD; P01295; His binding; 1.	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RA	Passeb G.C., Adams P.L., Harlos K., Nuttall P.A., Stuart D.I., NCBI_TaxID=34631;	Passeb G.C., Adams P.L., Harlos K., Nuttall P.A., Stuart D.I., NCBI_TaxID=34631;	RA	Passeb G.C., Adams P.L., Harlos K., Nuttall P.A., Stuart D.I., NCBI_TaxID=34631;	RA																																																																																																																																																																																																																																																																																																																																																																																																																																																				
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RESULT 6

HTTPG\_BORBU STANDARD; PRT; 616 AA.

ID HTTPG\_BORBU

AC P42555; 118 FOYGKVNIRNAE-----YQVGGGLNITDIFTDGLCDPYVEMADOCELWTK- 169

DT 01-OCT-1995 (Rel. 32, Created)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chaperone protein httpg (Heat shock protein httpg) (High temperature protein G)

GN HTTPG OR BB0560.

OS *Borrelia burgdorferi* (Lyme disease spirochete).

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Borrelia*.

NCBI\_TaxID=139; [1]

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 35210 / B31; [3]

RX MEDLINE=98065943; PubMed=9403685;

RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., Hickey E.K., Gwinn M., Lathigra R., White O., Ketchum K.A., Dodson R., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., Utterback T., Watshay L., McDonald L., Artiach P., Bowman C., Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., Smith H.O., Venter J.C., "Genomic sequence of a Lyme disease spirochete, *Borrelia burgdorferi*," *Nature* 390:580-586 (1997).

RN [4]

RP SEQUENCE OF 497-574 FROM N.A.

RX MEDLINE=95111614; PubMed=7812434;

RA Ojaimi C., Davidson B.E., Saint-Girons I., Old I.G.; "Conservation of gene arrangement and an unusual organization of rRNA genes in the linear chromosomes of the Lyme disease spirochaetes *Borrelia burgdorferi*, B. *Garnini* and B. *afzelii*," *Microbiology* 140:2931-2940 (1994).

CC -!- FUNCTION Molecular chaperone. Has ATPase activity (By similarity).

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the heat shock protein 90 family.

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CC DR HAMAP; MF\_00505; -!- 1.

CC DR InterPro; IPR003594; ATPbind\_ATPase.

CC DR InterPro; IPR001404; Hsp90.

CC DR Pfam; PF02558; Hspase\_c; 1.

CC DR PRINTS; PRO0183; Hsp90; 2.

CC DR PRINTS; PRO075; HEATSHOCK90.

CC DR SMART; SNO0387; Hspase\_c; 1.

CC DR PROSITE; PS00298; HSP90; 1.

CC KW Chaperone; ATP-binding; Heat shock; Complete proteome.

CC FT DOMAIN 1 333 542 B (BY SIMILARITY).

CC FT DOMAIN 334 543 615 C.

CC FT DOMAIN 543 616 AA; 71218 NW; D57652F8DBE84 CRC64;

Query Match 8.5%; Score 96; DB 1; Length 616;

Best Local Similarity 21.5%; Pseq. No. 0.69; Mismatches 92; Indels 42; Gaps 8;

Matches 46; Conservative 34; Mismatches 92; Indels 42; Gaps 8;

Db 121 FYSAPIVSERKVEVTSKKALESDAYIWSDSGKTYGTELEKAKKESEGTIEKLYNKEGL-- 178

QY 68 TGSWSQFKCLQV-----QETERKESEDTYVTSVIFRNA 101

Db 179 --TANKWIKIQBETIKKYSNHNINPIYKYSERPIKTKQKQEGIEBEKBLNTALWTWN- 234

QY 102 SSPIKINVTETKAVFQGYKVNRAEYQVGGLNITDIFTDGLCDPYVFNADQ 161

Db 235 KSEIKAEEENFVFTN-TFDYENPLMIHTKAGNIEYTYNLFYVPSKAPYDLY-PNTKP 292

QY 162 GCEIWKV--SHYKVPDCTFVNFWFCAD 190

Db 293 GVKLPINRIFITDSEGSILPNVLRFIKGIDQD 326

RESULT 7

HTTPG\_TREPA STANDARD; PRT; 639 AA.

ID HTTPG\_TREPA

AC P03919; 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DE Chaperone protein httpg (Heat shock protein httpg) (High temperature protein G).

GN HTTPG OR TP0984.

OS *Treponema pallidum*.

OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; *Treponema*.

NCBI\_TaxID=160; [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Nichols;

RX MEDLINE=8332770; PubMed=9665875;

RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McDonald M.P., Salzberg S., Peterson J., Utterback T., Khaliq H., Richardson D., Howell J.K., Chindambaran M., McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C., "Complete genome sequence of *Treponema pallidum*, the syphilis spirochete," *Science* 281:375-388 (1998).

CC DR -!- FUNCTION: Molecular chaperone. Has ATPase activity (By similarity).

CC DR -!- SUBUNIT: Homodimer (By similarity).

CC DR -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC CC -!- SIMILARITY: Belongs to the heat shock protein 90 family.

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CC DR U51879; AA97469; 1; -!- ALT\_INIT.

CC DR EMBL; AA00157; AAC6619.1; ALT\_INIT.

CC DR EMBL; L32145; AAC41403; 1; -.

CC DR HSPR; 207900; LYER.

CC DR TIGR; BB0560; -.





Db	194 DELHDYTSKIRELVKKYSDP <sup>+</sup> AWPIRMEVERRAPATSDGEGADGEEQVITQTI-N	251	QY	66 NDTDGSWASQFKC1QVQBIERKEEDYTVTSVFTFRNASSPIKYVW---TETVKAVFOY	120
QY	101 ASSPKYYVNTTETVKAVFOYQGYKINRMA-----IEYQVGGINNTIDTLIF	145	Db	187 DH-----FRUKHIVVSYSDHIAVPIYFCBAGNEIQNSASALWTRPSEILED	236
Db	252 SMKALWTKSKDEVSDEVEKFYKHLAHAWDDPLEVIAKAGTFFEQ-----ALIF	302	QY	121 GYRNTRNAIEQWG-----GGINNTDULIFTDGLCDVYVPNADQGCELWVK	169
QY	146 TDGELCDVTVTUPNADQGELWVKSHY----KHPYCTPVENVCAKD 190		Db	237 QFKEFYKSLSKAVDDPWTLNNEGAETNLILIPSSKTFDIFH-PKPKKTVLXKR	295
Db	303 TPSHAPPDFLNSDAKIGMOLYVKEFIMSDCDQMLPMLRFVKGVDAAED 352		QY	170 ----SHYKHVPDYCCTPVENVCAKD 190	
RESULT 10			Db	296 VFISDENIDLIPSYLRLRGVVDSED 321	
HTPG_RICPR	STANDARD;	PRT;	RC	NPBI_TaxID:187420;	
ID_HTPG_RICPR			RC	SEQUENCE FROM N.A.	
AC_Q9ZB9;			RC	STRAIN=Madrid; E;	
DT_30-MAY-2000	(Rel. 39, Created)		RC	MEDLINE=99039499; PubMed=9823893;	
DT_30-MAY-2000	(Rel. 39, Last sequence update)		RC	RA Andersson S.G.E., Zomorodipoor A., Andersson J.O.,	
DE_Chaperone protein	htpp (Heat shock protein https)	(High temperature	RA	Sichiretti-Ponten T., Almemark U.C.M., Podowski R.M., Naelund A.K.,	
DE_protein G1)			RA	Eriksson A.-S., Winkler H.H., Kurland C.G.,	
GN_HTPG OR RP840.			RA	"The genome sequence of Rickettsia prowazekii and the origin of	
OS_Rickettsia prowazekii.			RT	mitochondria,"; Nature 396:13-140(1998)	
OC_Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;			RL	CC -- FUNCTION: Molecular chaperone. Has ATPase activity (By	
OC_Rickettsiaceae; Rickettsiae; Rickettsia.			CC	similarity).	
OX_NCBI_TaxID=782;			CC	-- SUBUNIT: Homodimer (By similarity).	
RN_11			CC	-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).	
RP_SEQUENCE FROM N.A.			CC	-- SIMILARITY: Belongs to the heat shock protein 90 family.	
RC_STRAIN=Madrid; E;			CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
RX_MEDLINE=99039499; PubMed=9823893;			CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
RA_Sichiretti-Ponten T., Almemark U.C.M., Podowski R.M., Naelund A.K.,			CC	the European Bioinformatics Institute. There are no restrictions on its	
RA_Eriksson A.-S., Winkler H.H., Kurland C.G.,			CC	use by non-profit institutions as long as its content is in no way	
RA_HTPG OR RP840.			CC	modified and this statement is not removed. Usage by and for commercial/	
RA_Medline 99039499; PubMed 9823893;			CC	or send an email to license@ibb-sib.ch).	
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RA_Medline 99039499; PubMed 9823893;			CC	-----	
DR_EMBS_A2335273; CAIA15264.1; -			CC	-----	
DR_PIR; H71645; H71645.			CC	-----	
DR_HSSP; P02829; 1A4H.			CC	-----	
DR_HMABP; MF_0035; -; 1.			CC	-----	
DR_InterPro; IPR0359; ATPbind_ATPase.			CC	-----	
DR_InterPro; IPR0140; HP90.			CC	-----	
DR_Pfam; PF02518; HATPase_c; 1.			CC	-----	
DR_Pfam; PF00183; HSP90; 2.			CC	-----	
DR_PRINTS; PRO075; HATSOCK90.			CC	-----	
DR_SMART; SM0038; HATPase_c; 1.			CC	-----	
DR_PROSITE; PS00298; HSP90; 1.			CC	-----	
DR_Chaperone; ATP-binding; Heat shock; Complete proteome.			CC	-----	
DR_DOMAIN; 328; B (BY SIMILARITY).			CC	-----	
FT_DOMAIN; 329; 544			CC	-----	
SQ_SEQUENCE 621 AA; 70713 MW; 9797B97801524007 CRC64;			CC	-----	
Query Match 7.5%; Score 84.5; DB 1; Length 621;			CC	-----	
Best Local Similarity 18.9%; Pred. No. 7.3; Matches 39; Conservative 42; Mismatches 88; Indels 37; Gaps 8;			CC	-----	
QY 11 FVSAALATOETSAKAGENPLWAH-B-LILGYQ--QDAWKS-IDQGSVTVLAKT--TIVB	65		CC	-----	
Db 127 YSSFMVADKVTVTSRKAGESKVHTWESDGLGEVIVADSEOEFTTRGIVLYVIKSKETTEL	186		CC	-----	
QY 66 NDTDGSWASQFKC1QVQBIERKEEDYTVTSVFTFRNASSPIKYVW---TETVKAVFOY	120		QY	5 VVILITFSAALATOETSAKAGENPLWAH-B-LILGYQ--QDAWKS-IDQGSVTVLAKT--TIVB	64
Db 187 DH-----FRUKHIVVSYSDHIAVPIYFCBAGNEIQNSASALWTRPSEILED	236		Db	10 VVILITFSAALATOETSAKAGENPLWAH-B-LILGYQ--QDAWKS-IDQGSVTVLAKT--TIVB	169
QY 121 GYRNTRNAIEQWG-----GGINNTDULIFTDGLCDVYVPNADQGCELWVK	169		Db	10 VVILITFSAALATOETSAKAGENPLWAH-B-LILGYQ--QDAWKS-IDQGSVTVLAKT--TIVB	295
Db 237 QFKEFYKSLSKAVDDPWTLNNEGAETNLILIPSSKTFDIFH-PKPKKTVLXKR	295		QY	11 FVSAALATOETSAKAGENPLWAH-B-LILGYQ--QDAWKS-IDQGSVTVLAKT--TIVB	123
Db 170 ----SHYKHVPDYCCTPVENVCAKD 190			QY	65 ENTDGSWASQFKC1QVQBIERKEEDYTVTSVFTFRNASSPIK-YVNTETVKAVFOYGYK	123
Db 296 VFISDENIDLIPSYLRLRGVVDSED 321			QY	127 YSSFMVADKVTVTSRKAGESKVHTWESDGLGEVIVADSEOEFTTRGIVLYVIKSKETTEL	186





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Search completed: March 9, 2004, 13:34:32  
Job time : 20 SECS



Db	121 GYKRNWALIEYQGGGLNITDILIFTGELCDVFVVPNADQGCELMWIKSKHVKHVPDYCT 180
Qy	181 FVENVFCAKDRKTYDIFNEBCVNGEPWL 209
Db	181 FVENVFCAKDRKTYDIFNEBCVNGEPWL 209
RESULT 2	
Q8WV98	PRELIMINARY; PRT; 210 AA.
ID	Q8WV98: 01-OCT-2002 (TREMBrel. 22, Created)
AC	01-OCT-2002 (TREMBrel. 22, Last sequence update)
DT	01-OCT-2002 (TREMBrel. 22, Last annotation update)
DE	Putative 22.5 kDa secreted protein.
OS	Ixodes scapularis (Black-legged tick) (Deer tick).
OC	Bukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Ixodes; Ixodes; NCBI_TaxID=6945; [1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Rhode Island; TISSUE=Salivary gland;
RA	Mather T.N., Ribeiro J.M.C.;
RT	"Exploring the Sialome of the Tick Vector of Lyme Disease, Ixodes scapularis," to the EMBL/Genbank/DBJ database.
DR	EMBL; AF483717; AACM93664.1; -.
SQ	SEQUENCE 210 AA; C5B75614649A9BED CRC64;
Query Match	11.2%; Score 126; DB 5; Length 210;
Best Local Similarity	24.3%; Pred. No. 0.0029;
Matches	53; Conservative 41; Mismatches 90; Indels 34; Gaps 12;
AC	Q81979: 01-MAR-2003 (TREMBrel. 23, Created)
DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)
DE	Putative 22.5 kDa secreted protein.
OS	Bukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Ixodes; Ixodes; NCBI_TaxID=6945; [1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Rhode Island; TISSUE=Salivary gland;
RA	Mather T.N., Ribeiro J.M.C., Pham V.M., Garfield M.,
RT	"Exploring the Sialome of the Tick Vector of Lyme Disease, Ixodes scapularis," to the EMBL/Genbank/DBJ database.
DR	EMBL; AF483717; AACM93664.1; -.
SQ	SEQUENCE 210 AA; C5B75614649A9BED CRC64;
Query Match	11.2%; Score 126; DB 5; Length 210;
Best Local Similarity	24.3%; Pred. No. 0.0029;
Matches	53; Conservative 41; Mismatches 90; Indels 34; Gaps 12;
AC	Q81979: 01-MAR-2003 (TREMBrel. 23, Created)
DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)
DE	Putative 22.5 kDa secreted protein.
OS	Bukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Ixodes; Ixodes; NCBI_TaxID=6945; [1]
RESULT 3	
Q8WV93	PRELIMINARY; PRT; 306 AA.
ID	Q8WV93: 01-OCT-2002 (TREMBrel. 22, Created)
AC	01-OCT-2002 (TREMBrel. 22, Last sequence update)
DT	01-OCT-2002 (TREMBrel. 22, Last annotation update)
DE	Putative secreted histamine binding protein.
OS	Ixodes scapularis (Black-legged tick) (Deer tick).
OC	Bukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Ixodes; Ixodes; NCBI_TaxID=6945; [1]
RN	SEQUENCE FROM N.A.
RC	STRAIN=Rhode Island; TISSUE=Salivary gland;
RA	Valenzuela J.G., Francischetti I.M., Pham V.M., Garfield M., Mather T.N., Ribeiro J.M.C.;
RT	"Exploring the Sialome of the Tick Vector of Lyme Disease, Ixodes scapularis," to the EMBL/Genbank/DBJ database.
DR	EMBL; AF483717; AACM93639.1; -.
SQ	SEQUENCE 306 AA; 34232 MW; B2B09181CC395D CRC64;
Query Match	10.4%; Score 117.5; DB 5; Length 306;
Best Local Similarity	20.0%; Pred. No. 0.027;
Matches	46; Conservative 34; Mismatches 73; Indels 77; Gaps 7;
AC	Q8WV93: 01-OCT-2002 (TREMBrel. 22, Created)
DT	01-OCT-2002 (TREMBrel. 22, Last sequence update)
DE	Putative 22.5 kDa secreted protein.
OS	Ixodes scapularis (Black-legged tick) (Deer tick).
OC	Bukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Ixodes; Ixodes; NCBI_TaxID=6945; [1]
RESULT 4	
Q81979	PRELIMINARY; PRT; 176 AA.
ID	Q81979: 01-MAR-2003 (TREMBrel. 23, Created)
AC	01-MAR-2003 (TREMBrel. 23, Last sequence update)
DT	01-MAR-2003 (TREMBrel. 23, Last annotation update)
DE	TSGP4.
OS	Ornithodoros savignyi.
OC	Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Argasidae; Ornithodoros.
OC	NCBI_TaxID=69826; [1]
RN	SEQUENCE FROM N.A.
RC	TISSUE=Salivary gland;
RA	Nans B.J., Venter J.D., Vrey P.J., Louw A.I., Neitz A.W.;
RT	"Identification of putative Proteins involved in granule biogenesis of tick salivary glands."
RL	Electrophoresis 22:1739-1746 (2001).
DR	EMBL; AF428891; AACM93631.1; -.
SQ	SEQUENCE 176 AA; 19375 MW; 44B7559F3BCB6A25 CRC64;
Query Match	9.9%; Score 111.5; DB 5; Length 176;
Best Local Similarity	19.2%; Pred. No. 0.044;
Matches	30; Conservative 33; Mismatches 64; Indels 29; Gaps 6;
AC	Q81979: 01-MAR-2003 (TREMBrel. 23, Created)
DT	01-MAR-2003 (TREMBrel. 23, Last sequence update)
DE	Putative secreted histamine binding protein.
OS	Ixodes scapularis (Black-legged tick) (Deer tick).
OC	Bukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Ixodes; Ixodes; NCBI_TaxID=6945; [1]
RESULT 5	
Q8WV92	PRELIMINARY; PRT; 311 AA.
ID	Q8WV92: 01-OCT-2002 (TREMBrel. 22, Created)
AC	01-OCT-2002 (TREMBrel. 22, Last sequence update)
DT	01-OCT-2002 (TREMBrel. 22, Last annotation update)
DE	Putative secreted histamine binding protein.
OS	Ixodes scapularis (Black-legged tick) (Deer tick).
OC	Bukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari; Parasitiformes; Ixodida; Ixodes; Ixodes; NCBI_TaxID=6945; [1]

OX NCBI\_TaxID=6945;  
 RN [1] SQUENCE FROM N.A.  
 RP STRAIN=Rhode Island; TISSUE=Salivary gland;  
 RC Valenzuela J.G., Francischetti I.M., Pham V.M., Garfield M.,  
 RA Mather T.N., Ribeiro J.M.C.;  
 RT "Exploring the Sialome of the Tick Vector of Lyme Disease, *Ixodes*  
 RT *scapularis*," (FEB-2002) to the EMBL/GenBank/DBTA databases.  
 DR EMBL; AF483718; AAM91640; 1; -.  
 DR SEQUENCE 311 AA; 3651 MW; D7E329FEE4CF19A CRC64;  
 SQ

Query Match 9.2%; Score 103; DB 5; Length 311;  
 Best Local Similarity 19.6%; Pred. No. 0-54; 79; Indels 128; Gaps 12;  
 Matches 59; Conservative 35; Mismatches 51;

QY 12 VSAALATQAEITISAKAGENPLWAHEELIGKYQDAWKSIDOGUSVWVLAKEYTENDTSSW 71  
 DB 13 VSAAKAYEVFQSDRAPPDNPDALKOLGAMQDAWAKTIFTAHNSYLYSS----GW 66

QY 72 GSQ---FKCLQVOEYERKEEVDYTTSVFTRNASSPIKYN-----VITYKAVF 118  
 DB 67 GTEBHYEDVRCLOQVHSSDN-----YILKSAATSKWYNTSKRMSSTQVYQAK 117

QY 119 Q-YGYKNTR-----NAIEQV-----GGGNI-----TDTI 144  
 DB 118 QKYSIENIMHUGQPREVTSNGTCYMLNFTCLSGGGRHHCWQWRKTYKSYKV 177

QY 145 FTDQELCDYFVYENADQG--CEBW-----VKSASH--- 171

DB 178 LFSTPLCITYVRSI-QDDEGYESCPFWLSEDWIKKNTVTPQVUVTIHKEDSDEIERSEREE 237

QY 172 -----YKHPDYCYPVNFCA-----KDRKTYDIFN 198

DB 238 SYRKESVOCEEPRANKTFLYDILFKEDPSSCCKYAFLINCGYKPYRKYDQKDDKIN 297

QY 199 E 199

DB 298 E 298

RESULT 6

ID Q837S0 PRELIMINARY; PRT; 722 AA.  
 AC Q837S0;  
 DT 01-JUN-2003 (TREMBREL. 24, Created)  
 DT 01-OCT-2003 (TREMBREL. 25, Last annotation update)  
 DE Amino acid ABC transporter, amino acid-binding/permease protein.  
 GN EF0761.  
 OS *Enterococcus faecalis* (Striptococcus faecalis).  
 OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
 NCBI\_TaxID=1351;  
 RN [1] SEQUENCE FROM N.A.  
 RP STRAIN=VS83 / ATCC 700802;  
 RX MEDLINE:2255987; PubMed:12663927;  
 RA Pausen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,  
 RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,  
 RA Tettelin H., Dodon R.J., Umayam L., Brinkac L., Beaman M., Nelson W.,  
 RA Daubert S., Deboy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,  
 RA Vamathevan J., Tran B., Hansen T., Shetty J., Khouri H.,  
 RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.,  
 RT "Role of mobile DNA in the evolution of vancomycin-resistant  
 RT Enterococcus faecalis,"  
 RT Entercoccus faecalis;  
 RL Science 299:7071-7074(2003).  
 DR EMBL; AB16949; AAO8058; 1; -.  
 DR TIGR; EF0761; -.  
 DR GO; GO:003028; C:membrane; IEA.  
 DR GO; GO:0005234; :Glutamate-gated ion channel activity; IEA.  
 DR GO; GO:0004970; F:transporter activity; IEA.  
 DR GO; GO:0005215; F:transporter activity; IEA.

DR GO; GO:0006810; Pitransport; IEA.  
 DR InterPro; IPR000515; BPD\_transp.  
 DR InterPro; IPR001320; Ion\_glu\_receptor.  
 DR InterPro; IPR001311; SBP\_glu\_receptor.  
 DR InterPro; IPR001639; SBP\_bac\_3.  
 DR Pfam; PF00528; BPD\_transp; 1.  
 DR Pfam; PF00497; SBP\_bac\_3; 2.  
 DR SMART; SM0079; PBIE; 1.  
 DR PROSITE; PS00402; BPD\_TRANSPINN\_MEMBR; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 722 AA; 79713 MW; D7F763B20BDE62 CRC64;

Query Match 9.1%; Score 102.5; DB 16; Length 722;  
 Best Local Similarity 26.9%; Pred. No. 1-8; 72; Indels 65; Gaps 15;  
 Matches 60; Conservative 26; Mismatches 51;

QY 16 LATQATTSAA----KAGENPLWAHEELIGKYQDAWKSIDOGUSVWVLAKEYT-----TETVKA 116  
 DB 204 LVGKDEKGSSGFGAVKKGQNP----ELIKKPNAGLKLQKONG--TVDKILNLYLATGD 255

QY 65 ENDTSWSGSPKCLQVOEYERKEEVDYTTSVFTRNASSPIKYN-----TETVKA 116  
 DB 256 ETNTQDAGEONK----KTRPKKEKVKVIALDSTF---APFEFONAQSDYVGIDVDLVRR 306

QY 117 V-----FQY-GKVNRAAEM-QVGG---GNIIDTLIFPGECLDVFVTPNADQ 162  
 DB 307 AAELQGFTVSPFKF1GSSAVQAVVSGQADGMVACTITD---DRKQAFDFSVPYFBSG 361

QY 163 CEIWKVSKH--YKHPDYCYPVNFCA-----FCAKRTYD 195  
 DB 362 IQIAVKEGNDKIKSYDLDKQKVKYKIGTESADPFLERKNKQYD 404

RESULT 7

ID Q95WZ5 PRELIMINARY; PRT; 221 AA.  
 AC Q95WZ5;  
 DT 01-DEC-2001 (TREMBREL. 19, Created)  
 DT 01-DEC-2001 (TREMBREL. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBREL. 22, Last annotation update)  
 DE Histamine binding protein.  
 GN HBP.  
 OS *Ixodes scapularis* (Black-legged tick) (Deer tick).  
 OC Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Acari;  
 OC Paracitomes; Ixodida; Ixodidae; Ixodes.  
 OX NCBI\_TaxID=6945;  
 RN [1] SQUENCE FROM N.A.  
 RP SEQUENCE FROM N.A.  
 RA Das S., Banerjee G., DePonte K., Marcantonio N., Kantor F.S.,  
 RA Fikrig E.;  
 RT "Salp3D, an *Ixodes scapularis* antioxidant, is one of 14  
 RT immunodominant antigens in engorged tick salivary glands.,"  
 RL Infect. Dis. 184:10-0(2001).  
 DR EMBL; AF203913; AAK07816; 1.  
 SQ SEQUENCE 221 AA; 25359 MW; 7B995AC9C0AFA252 CRC64;

Query Match 8.7%; Score 97.5; DB 5; Length 221;  
 Best Local Similarity 23.4%; Pred. No. 1-1; 80; Indels 37; Gaps 14;  
 Matches 49; Conservative 43; Mismatches 51;

QY 10 TFSVAAALQAE-----TSAKAGENPLWAHEELIGKY-QDAWKSIDOGUSVWVIA 60  
 DB 31 TKGSTGTTTTRGPRGARMVITAPPEDP-----SKRQEQAIRVVE-MATQWIK 80

QY 61 KTYTENDTGSWSQKQLOQVBEIREEKDVTYV-FTRNASSPIKYN-----VKA 117  
 DB 81 WRYTYD-VTDESGNPVQCNFMRK-----TPTVNSPQVYKSN-SWETIDETILKDI 134

QY 118 FQGYKRNATEFQVQGGINITD-FDGEGLDVFVTPNADG--CEIWKVSKH-- 172  
 DB 135 GERGFPAVWVNFRTPIG--IATDNLVLYSNVYNTVLRIPPTNGERHCDLWANLTS 191



Query Match 7.6%; Score 86; DB 16; Length 399;  
 Best Local Similarity 23.8%; Pred. No. 24; Mismatches 37; Indels 38; Gaps 4;  
 Matches 30; Conservative 21; Mismatches 37; Indels 38; Gaps 4;

QY 42 YQDDAWSK--IDQG-----VSTIVLAKTTVENDTSWSQPKCLOQVEIER 85  
 Db 224 YERAKKSLEYIESGENFLMSRYSYENIEMNLSFSRIRETNNSNIKASYKEAFKALSMIDM-- 281

QY 86 KEDDVITVSVFPRRASPIKIVV-----NIVKAVFOQSKRANIALEQVGGL 137  
 Db 282 -----YDNDSKIKNENLGIIRIFIELAEIKDVKHQCYENIGPILEDKSHM 329

QY 138 NTIDTL 143  
 Db 330 NLIDTL 335

RESULT 13

ID Q51717 PRELIMINARY; PRT; 584 AA.  
 AC 51717;  
 DR 01-NOV-1996 (TREMBrel. 01, Created)  
 DT 01-DEC-2001 (TREMBrel. 19, Last sequence update)  
 RT 01-OCT-2003 (TREMBrel. 25, Last annotation update)  
 DE Hypothetical protein precursor.  
 OS Pseudomonas fluorescens.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomadaceae; Pseudomonas.  
 RN [1]  
 RX NCBI\_TAXID=294;

Query Match 7.7%; Score 86.5; DB 16; Length 932;  
 Best Local Similarity 25.5%; Pred. No. 68; Mismatches 47; Indels 49; Gaps 11;  
 Matches 41; Conservative 24; Mismatches 47; Indels 49; Gaps 11;

QY 44 DAWKSIDQGVSVTVLAKTTVENDTG---SWSQ---FKCLQ-QVIEERKEEDYTVTFV 96  
 Db 221 DGFKDIDRG-----GDTGFDLTDWGGKLGFRRTADGTQPFVKQYNTDTSNE 267

QY 97 TFRMAS-----SPKYYN-----VTEVKAVFOQYKVNRAIEQVGGGNNITDYLIF 145  
 Db 268 TYLGTLLDDPKDTPFRRTMASQKDVHAAHNTVQVYD-----SEITPDNLITTVYR 180

QY 146 TDG-----ELCDVTPVTPNADQGCBLLWVKKSHYHVPH-YCT 180

Db 321 TDTRPAWYKLNDV--RNDSITG--WVLSNLADPDTYR 320

RESULT 12

Q8XMD0 PRELIMINARY; PRT; 399 AA.  
 ID Q8XMD0 PRELIMINARY; PRT; 399 AA.  
 AC Q8XMD0; 2002 (TREMBrel. 20, Created)  
 DT 01-MAR-2002 (TREMBrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)  
 DR Hypothetical Protein CFB0759.

OS Clostridium perfringens  
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;  
 OC Clostridium;  
 OC NCBII\_TaxID=1502;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=13 / Type A;  
 RX MEDLINE=21563373; PubMed=11792842;  
 RN Shimizu T., Ohnani K., Hirakawa H., Ohshima K., Yamashita A.,  
 RA Shiba T., Ogawa N., Hattori M., Kuhara S., Hayashi H.,  
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic  
 RT flesh-eater.", Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).  
 DR EMBL; AP003188; BAB80455; 1; -;  
 KW Hypothetical protein; complete proteome.  
 SQ SEQUENCE FROM N.A.  
 MEDLINE=21396507; PubMed=11481430;

Query Match 7.6%; Score 86; DB 16; Length 399;  
 Best Local Similarity 23.8%; Pred. No. 24; Mismatches 37; Indels 38; Gaps 4;  
 Matches 30; Conservative 21; Mismatches 37; Indels 38; Gaps 4;

QY 39 LGKQDAWKSIDQGVSVTVLAKTTVENDTGWSQPKCLOQVEIER 91  
 Db 433 VGHLDGYREKOM-----YQASIAIYNFGVLAQDASATLFVLSVQGGLDVYDYE 487

QY 92 VTSVFTFRMASSPPKYYN-----VTEVKAVFOQYKVNRAIEQVGGGNN 138  
 Db 488 ATSTATGQAQSILQTYTNVNLNVPSFGYQYSINGVAPQLTNGID 534

RESULT 14

Q3983 PRELIMINARY; PRT; 917 AA.  
 ID Q3983  
 AC Q3983;  
 DT 01-JAN-1998 (TREMBrel. 05, Created)  
 DT 01-JAN-1998 (TREMBrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TREMBrel. 24, Last annotation update)  
 DR AMI.  
 GN AMI.  
 OS Listeria monocytogenes.  
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.  
 RX MEDLINE=9746036; PubMed=9282740;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 MEDLINE=9746036; PubMed=9282740;  
 RX Braun L., Damsi S., Dehoux P., Bierne H., Lindhal G., Cossart P.;

RT "InlB : an invasion protein of *Listeria monocytogenes* with a novel  
 RT type of surface association.";  
 RL Mol: Microbial; 25:285-294(1997).  
 DR EMBL; U82488; AAC4505.1; -.  
 GO; GO:0005745; P:N-acetyl-muramoyl-L-alanine amidase activity; IEA.  
 DR InterPro; IPR002502; Amidase\_2.  
 DR Pfam; PF0510; Amidase\_2; 1.  
 DR SMART; SM00644; Amidase\_2; 1.  
 SQ SEQUENCE 917 AA; 102352 MW; 21EA2452B4FF03B7 CRC64;

Query Match

Best Local Similarity 7.6%; Score 85.5; DB 2; Length 917;

Matches 38; Conservative 24; Mismatches 49; Indels 53; Gaps 9;

Search completed: March 9, 2004, 13:35:31

Job time : 50 secs

QY

Db 927 YVPNSQDEMPFVDITDKSGAITYSAVDAOKDFWDFVNDSVLLKDR-----GKVERNGS 981

QY 207 --PML 209

Db 982 LTPWI 986

QY 28 GNPMLWABEELLGKQYDAWKSIDQGVSVTYLAKTYEENDT--GSGWG-----S 73  
 Db 223 GKGTVWSHD-----AVTRVLLGHTHTDPVAVNQWGNFNRNFVSHNE 265  
 QY 74 QPKLQLQYQISTERKEEDYTVTSVFTFRNASSPPIKY--NVTETVKA--FQKQKNTR-- 126  
 DB 266 KIKAMQV-NIYEKEDRAKINRVSRAKNGSVWKPNTKEAKLVNPLISSGKRNRII 324  
 QY 127 -----NAIEQ--QGGGLNITDFTLIFTGELCVVYVPNADO 161  
 Db 325 REAKTSGGTIVQPSVGG-----KTIQWVDSKALNTFVTPSMEK 363

RESULT 15

Q8A812 PRELIMINARY; PRT; 1090 AA.

AC Q8A812; 1;

ID Q8A812; PRELIMINARY; PRT; 1090 AA.

DT 01-JUN-2003 (Tremblar). 24, Last sequence update

DT 01-OCT-2003 (Tremblar). 25, Last annotation update  
 DE OmpA-related protein.  
 GN B1185.OS Bacteroides thetaiotaomicron.  
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;  
 OC Bacteroidaceae; Bacteroides.  
 OC NCBI\_TaxID:818;  
 RN [1]

RP SEQUENCE FROM N A.

RC STRAIN=VPI-5482 / ATCC 29149;

RX MEDLINE=22550858; PubMed=2663928;

RA Chiang H.C., Hooper L.V., Gordon J.I.;

RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";  
 RL Science 295:2074-2076(2003).

DR EMBL; AE016930; AA076292.1; -.

DR GO; GO:004553; P:hydrolyase activity, hydrolyzing O-glycosyl . . . ; IEA.

DR GO; GO:005975; P:carbohydrate metabolism; IEA.

DR InterPro; IPR003969; Carboxypeptidase.

DR InterPro; IPR00164; Crystallin.

DR InterPro; IPR00111; Glyco\_hydro\_GHD.

DR ProdDom; PDO02572; Glyco\_hydro\_GHD; 1.

DR PROSITE; PS00225; CRYSTALLIN\_BETA1GAMMA; 1.

KW Complete proteome.

SQ SEQUENCE 1090 AA; 122044 MW; 63C8B3A1E8A2DFA6 CRC64;

Query Match 7.6%; Score 85.5; DB 16; Length 1090;  
 Best Local Similarity 23.8%; Pred. No. 1e+02; Mismatches 44; Conservative 19; Mismatches 41; Indels 41; Gaps 9;QY 47 KSIQG---VAVTIVLAKTYEN---DQSGWQDKLQVQDIERKEEDYTVTF 96  
 Db 821 KKYDPFGFPGSISGYTYWAKDITANPGSAPNSAWON--VAVNSINDPVGYSLSLSPHR 877QY 97 TFRMAMSPPIKTVNTETVKAFOQIGKRNRAIE--QVGGGLNITDFTLIFTGELCVF 154  
 Db 878 ITANASSTEINVAKCLKTFPSIYFSGHTGRGSVTTYNDNG-----DQNYSPIL 926

SQ 155 YVPNADQCEL-----WVKSHYKHPDYCTFVNFCAKDKRTYDFNBBCVNGE 206

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: March 9, 2004, 13:30:30 ; Search time 60 Seconds

Perfect score: 1125 US-09-555-296B-4  
Sequence: 1 MRNQVWILLTHVSAALATQA. .... DRKYDIDFNEBCTYNGEPWL 209

Scoring table: BLOSUM62 984.207 Million cell updates/sec  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2001s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003s:\*

7: geneseqp2003s:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

\* Query

Result No. Score Match Length DB ID Description

Result No.	Score	Match	Length	DB	ID	Description
1	1125	100.0	209	2	AAM37449	Aaw37449 Tick vaso
2	1125	100.0	209	2	AAY18081	Aay18081 Histamine
3	364	32.4	203	2	AAY18086	Aay18086 Histamine
4	353	31.4	203	2	AAY18085	Aay18085 Histamine
5	290.5	25.8	190	2	AAM71447	Aaw37447 Tick vaso
6	290.5	25.8	190	2	AAY18079	Aay18079 Histamine
7	284.5	25.3	198	2	AAY18084	Aay18084 Histamine
8	282	25.1	171	4	AAB73261	Aab73261 Histocali
9	282	25.1	171	4	AAB74289	Aab74289 Histocali
10	265	23.6	200	2	AAM37448	Aaw37448 Tick vaso
11	265	23.6	200	2	AAY18080	Aay18080 Histamine
12	252	22.4	190	2	AAM71446	Aaw37446 Tick vaso
13	252	22.4	190	2	AAY18078	Aay18078 Histamine
14	251.5	22.4	182	4	AAB73262	Aab73262 Histocali
15	251.5	22.4	182	4	AAB74290	Aab74290 Histocali
16	239	21.2	172	4	AAB73260	Aab73260 Histocali
17	239	21.2	172	4	AAB74288	Aab74288 Histocali
18	140	12.4	284	2	AAY18088	Aay18088 Histamine
19	127.5	11.3	285	2	AAY18087	Aay18087 Histamine
20	126.5	9.1	321	2	AAY18089	Aay18089 Histamine
21	102.5	8.7	722	4	AAY15203	Aay15203 Enterococ
22	97.5	8.7	221	4	AAY7764	Aay7764
23	96	8.5	6	ABU19265	Abu19265 protein e	
24	91	8.1	202	2	ABU37467	Aar37467 Sequence
25	7.8		88	6	ABU33830	Abu33830 Protein e

ALIGNMENTS

Abu48728 Protein e  
Ab55683 Drosophil  
Aag7991 Arabidops  
Abg03896 Novel hum  
Aag77990 Arabidops  
Aag77989 Arabidops  
Abu5973 Protein e  
Abu29629 Protein e  
Aac5562 B. faeciu  
Abb8437 Listeria  
Aay7773 I. scapul  
Aay18083 Histamine  
Aaw8149 Bacillus  
Aaw20536 H. pylori

Abb6456 Drosophil  
Abu0485 Protein e  
Abu1213 Protease  
Aaw4121 Thermococ  
Aaw9440 Wobetox  
Aaw9440 W. pylori

Raw0536

Database : A\_Geneseq\_29Jan04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2001s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003s:\*

7: geneseqp2003s:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

\* Query

Result No.

Score

Match

Length

DB

ID

Description

XX

CC identified. The VABPs can be expressed in host cells using e.g. a  
 CC baculovirus expression system. They can be used: (i) to assay histamine  
 CC (or other VA such as serotonin) in body fluids or cell culture  
 CC supernatants, e.g. to monitor the effect of allergens; (ii) for binding  
 VA, e.g. to remove histamine from blood, food, cell cultures etc.; (iii)  
 CC as an antihistamine or anti-inflammatory agents, e.g. for treating slow  
 CC insect, snake or scorpion bites or dermatitis, or as a carrier for slow  
 CC release of histamine-related compounds; (iv) in vaccines to protect  
 CC against merozoite parasites, especially in animals; (v) as reagents for  
 CC studying inflammation, involvement of VA in ulcer formation or the immune  
 CC response etc. VABPs provide a more sensitive assay for histamine than low  
 CC -affinity antibodies currently used. They may also be more effective and  
 CC safer than conventional antihistamines. (Updated on 27-AUG-2003 to  
 CC correct OS field.)  
 XX

SQ Sequence 209 AA;

Query Match 100.0%; Score 1125; DB 2; Length 209;

Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMQCVVLLTTFVSAALATOETTSAKAGENPLWAEELIGKQDAWKSIDQGVSYTVLA 60  
 Db 1 MMQCVVLLTTFVSAALATOETTSAKAGENPLWAEELIGKQDAWKSIDQGVSYTVLA 60  
 QY 51 KTYTENDGSMQSOPKLCQVPIERKEEDYTVTSTERNASSPITKVNNTETKAVFOY 120  
 Db 61 KTYTENDGSMQSOPKLCQVPIERKEEDYTVTSTERNASSPITKVNNTETKAVFOY 120  
 QY 121 GYKNTRNATEQVQGGNNITDTIFTDGLCDVYVNAQDGCELMWVKSHYKHPDYCT 180  
 Db 121 GYKNTRNATEQVQGGNNITDTIFTDGLCDVYVNAQDGCELMWVKSHYKHPDYCT 180  
 QY 181 FVFNVFCAKDRKTYDIFNEECVYNGEPWL 209  
 Db 181 FVFNVFCAKDRKTYDIFNEECVYNGEPWL 209

RESULT 2

ID AAY18081  
 AC AAY18081 standard; protein; 209 AA.

XX

AC AAY18081;

XX

DT 06-AUG-1999 (first entry)

XX

DS Histamine binding protein D.RET6.

XX

KW Histamine binding protein; serotonin binding compound; inflammation;

KW gastric acid secretion; allergy; type I hypersensitivity reaction;

KW asthma; urticaria; allergic rhinitis; food allergy;

KW drug allergy; abnormal blood pressure; psychological disorder; vaccine;

KW respiratory disease; coronary heart disease; cellular growth regulator;

KW tissue repair; blood-sucking ectoparasite; therapy.

Rhipicephalus appendiculatus.

XX

PN W09927104-A1.

XX

PD 03-JUN-1999.

XX

PF 26-NOV-1998; 98WO-GB003530.

XX

PR 26-NOV-1997; 97GB-00025046.

XX

PR 26-JUN-1998; 98GB-00013917.

XX

(OXFO-) OXFORD VACS LTD.

XX

PT Nuttall PA, Paeser GC;

XX

DR WPI; 1999-357841/30.

XX

N-FSDB; AAX76967.

XX

PT Histamine and serotonin binding compounds useful for the treatment of

PT allergies.

XX

PS

Claim 1; Fig 4; 84pp; English.

XX

CC This sequence is an example of a histamine or serotonin binding compound  
 CC (A), of the invention. The compounds are useful for regulating the action  
 CC of histamine and serotonin (in e.g. inflammation and gastric acid  
 CC secretion), the detection, quantification and removal of histamine or  
 CC serotonin in animals, plants, cell cultures, food materials, or humans)  
 CC and in the treatment of various diseases and allergies (e.g. type I  
 CC hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay  
 fever), atopic dermatitis, insect bites and food and drug allergies,  
 CC abnormal blood pressure, migraine, psychological disorders, respiratory  
 CC disease, and coronary heart disease). Histamine may also be used to  
 CC regulate cellular growth and tissue repair. The molecules may also be  
 CC used as components of vaccines directed against blood-sucking  
 XX

SQ Sequence 209 AA;

Query Match 100.0%; Score 1125; DB 2; Length 209;

Matches 209; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMQCVVLLTTFVSAALATOETTSAKAGENPLWAEELIGKQDAWKSIDQGVSYTVLA 60  
 Db 1 MMQCVVLLTTFVSAALATOETTSAKAGENPLWAEELIGKQDAWKSIDQGVSYTVLA 60  
 QY 61 KTYTENDGSMQSOPKLCQVPIERKEEDYTVTSTERNASSPITKVNNTETKAVFOY 120  
 Db 61 KTYTENDGSMQSOPKLCQVPIERKEEDYTVTSTERNASSPITKVNNTETKAVFOY 120  
 QY 121 GYKNTRNATEQVQGGNNITDTIFTDGLCDVYVNAQDGCELMWVKSHYKHPDYCT 180  
 Db 121 GYKNTRNATEQVQGGNNITDTIFTDGLCDVYVNAQDGCELMWVKSHYKHPDYCT 180  
 QY 181 FVFNVFCAKDRKTYDIFNEECVYNGEPWL 209  
 Db 181 FVFNVFCAKDRKTYDIFNEECVYNGEPWL 209

RESULT 3

ID AAY18086  
 AC AAY18086 standard; protein; 203 AA.

XX

AC AAY18086;

XX

DT 06-AUG-1999 (first entry)

XX

DS Histamine binding protein Th/Bm-HBP2.

XX

KW Histamine binding protein; serotonin binding compound; inflammation;

KW gastric acid secretion; allergy; type I hypersensitivity reaction;

KW asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy;

KW drug allergy; abnormal blood pressure; psychological disorder; vaccine;

KW respiratory disease; coronary heart disease; cellular growth regulator;

KW tissue repair; blood-sucking ectoparasite; therapy.

XX

OS Boophilus microplus.

OS Synthetic.

XX

PN W09927104-A1.

XX

PD 03-JUN-1999.

XX

PF 26-NOV-1998; 98WO-GB003530.

XX

PR 26-NOV-1997; 97GB-00025046.

XX

PR 26-JUN-1998; 98GB-00013917.

XX

(OXFO-) OXFORD VACS LTD.

XX

XX Nuttall PA, Paesen GC; PI 26-NOV-1998; 98WO-GB003530.  
 XX WPI; 1999-357841/30.  
 DR N-PSDB; AAX76971.  
 XX PT Histamine and serotonin binding compounds useful for the treatment of PT allergies.  
 XX  
 PS Claim 14; Fig 8; 84pp; English.  
 CC This sequence is an example of a histamine or serotonin binding compound (A), of the invention. cDNA encoding this sequence was isolated from a mixed *Boophilus microplus*/*Ixodes hexagonus* cDNA expression library. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking ectoparasites  
 SQ Sequence 203 AA;

Query Match 32.4%; Score 364; DB 2; Length 203;  
 Best Local Similarity 38.1%; Pred. No. 6 3e-28; Matches 75; Conservative 38; Mismatches 78; Indels 6; Gaps 5;  
 CC  
 QY 6 VVLLITFVSLALATOETTSAKAGENPLWAHEELIGKQDAWKSIDGCVSVTVLACVTE 65  
 DB 8 VVLLITAVTAADQAPPSSTRNEPLEKTTW-HNQITGRYQDAWKSINOSVGTVIYFLRSTY 66  
 CC  
 QY 66 NUDTGSWGSQPKCQVQERKEEDYTTSVFTNASSPPIKVNVTETVKAVFQVQYKNI 125  
 DB 67 NDS-WVGKNFTCLSVTVSKYESTP-TWENTYTKNQSQ-QWVSMSSBNVTAQOGY-SV 122  
 CC  
 QY 126 RNAIEQYQGGGLNITDILIFTDQGALCDYFIVNADQGCELMVWKKSKHXRVDIYCTFVNV 185  
 DB 123 KNITQIOWTENNTKNDPNTWVFTQGTCYDLYIYKEDGYELWRSSETLQNTTCCOFIDL 182  
 CC  
 QY 186 FCAKDRKTYDIFNEECV 202  
 DB 183 -VALGRTTYNISTPNCV 198  
 CC  
 RESULT 4  
 AAY18085  
 ID AAY18085 standard; protein; 203 AA.  
 XX  
 AC AAY18085;  
 XX  
 DT 06-AUG-1999 (first entry)  
 DE Histamine binding protein 1h/Bm-HBPI.  
 CC  
 KW Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.  
 XX  
 OS Boophilus microplus.  
 OS Ixodes hexagonus.  
 OS Synthetic.  
 XX  
 PN WO9927104-A1.  
 XX  
 PD 03-JUN-1999.

XX Nuttall PA, Paesen GC; PI 26-NOV-1998; 98WO-GB003530.  
 XX WPI; 1999-357841/30.  
 DR N-PSDB; AAX76970.  
 XX PT Histamine and serotonin binding compounds useful for the treatment of PT allergies.  
 XX  
 PS Claim 13; Fig 7; 84pp; English.  
 CC This sequence is an example of a histamine or serotonin binding compound (A), of the invention. cDNA encoding this sequence was isolated from a mixed *Boophilus microplus*/*Ixodes hexagonus* cDNA expression library. The compounds are useful for regulating the action of histamine and serotonin (in e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking ectoparasites  
 SQ Sequence 203 AA;

Query Match 31.4%; Score 353; DB 2; Length 203;  
 Best Local Similarity 36.3%; Pred. No. 7 8e-27; Matches 74; Conservative 41; Mismatches 81; Indels 8; Gaps 6;  
 CC  
 QY 1 MKMOMVYLLIPVSLALATOETTSAKAG--ENTLWAHEELIGKQDAWKSIDGCVSVTV 58  
 DB 1 MKALLIJIAVGVLAVTAADQAPPSSTRNEPLEKTTW-HNQITGRYQDAWKSINOSVG 59  
 CC  
 QY 59 LAKTYYDNGWSQPKCQVQERKEEDYTTSVFTNASSPPIKVNVTETVKAVF 118  
 DB 60 FLRSTYNNDS-WVGKNFTCLSVTVSKYESTP-TWENTYTKNQSQ-QWVSMSSBNVTAQ 116  
 CC  
 QY 119 QYGYKRNMAIEQYQGGGLNITDILIFTDQGALCDYFIVNADQGCELMVWKKSKHXR 178  
 DB 117 ERGY-DVKNTQWTTENNTKNDPNTWVFTQGTCYDLYIYKEDGYELWRSSETLQNT 175  
 CC  
 QY 179 CTFVENVFCARDKRYDIFNEECV 202  
 DB 176 CQFIFDL-VALGRTTYNISTPNCV 198  
 CC  
 RESULT 5  
 AAW37447  
 ID AAW37447 standard; protein; 190 AA.  
 XX  
 AC AAW37447;  
 XX  
 DT 08-JUN-1998 (first entry)  
 DE Tick vasoactive amine binding protein 2 F5-HBPI2.  
 XX  
 KW Female-specific vasoactive amine binding protein 1; F5-HBPI; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine; transgenic animal; tick.  
 XX  
 OS Rhipicephalus appendiculatus.  
 XX  
 FF Location/Qualifiers



AAV18084  
ID AAV18084 standard; protein; 198 AA.  
XX  
AC AAV18084;  
XX  
DT 06-AUG-1999 (first entry)  
XX  
DE Histamine binding protein Av-HBP.  
XX  
KW Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; KW respiratory disease; coronary heart disease; cellular growth regulator; KW tissue repair; blood-sucking ectoparasite; therapy.  
XX  
OS Amblyomma variegatum.  
XX  
WO927104-A1.  
XX  
PN  
PD 03-JUN-1999.  
XX  
PP 26-NOV-1998; 98WO-GB003530.  
XX  
PR 26-NOV-1997; 97GB-00025046.  
XX  
PR 26-JUN-1998; 98GB-00013917.  
XX  
PA (OXFO-) OXFORD VACS LTD.  
XX  
PA Nuttall PA, Paesen GC;  
XX  
WPI; 1999-357841/30.  
DR N-PSDB; AAX76969.  
XX  
PT Histamine and serotonin binding compounds useful for the treatment of allergies.  
PT Nuttall PA, Paesen GC;  
XX  
PS Claim 12; Fig 6; 84PP; English.  
XX  
CC This sequence is an example of a histamine or serotonin binding compound (A), of the invention. The compounds are useful for regulating the action of histamine and serotonin in e.g. inflammation and gastric acid secretion, the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking ectoparasites  
CC  
XX  
SQ Sequence 198 AA;  
Query Match 25.3%; Score 264.5; DB 2; Length 198;  
Best Local Similarity 35.4%; Pred. No. 5.2e-20;  
Matches 5; Conservative 36; Mismatches 63; Indels 7; Gaps 4;  
CC  
XX  
Qy 31 PLWAHEELIGKYQDKWSIDQGVSTVYLAKTYYENDTGWSWSQFKCQLQVQIERKEEDY 90  
Db 23 PTWADBEGRGFKIQWAKALMQRINTVHLVRSTIDNIPYLMKQFSCQARAVTEVPPSK 82  
Qy 91 TVTSTPFTERRASSPCKYKVNMTETKAVQYQGYKRNIRALEYQVGGGLNITDTLIFTGE 150  
Db 83 TVELPFSFRNTRGIGLQMRN--QTVRAGKDYFYHQ-PNAFEFLMRGNRSPSNAMVFDGWT 139  
Qy 151 CDVFTVPP--NADQCELMWVTKSKYKHPDPYCFVFNFCAKDR 191  
Db 140 CNLISPPYQYRNPQ-CELWVQDTRUDNIPPCCSFMDYLCQPR 182  
OS  
RESULT 9  
AA74289  
ID AAB74289 standard; protein; 171 AA.  
XX  
AC AAB74289;  
XX  
DT 20-JUN-2001 (first entry)  
XX  
DE Histacalin protein FS-HBP2.  
XX  
KW Histacalin; FS-HBPI; conjunctivitis.  
XX  
OS Unidentified.

XX WO200115719-A2. PN XX

PD 08-MAR-2001. PR XX

XX 24-AUG-2000; 2000WO-GB0013382. PR XX

XX 01-SEP-1999; 99GB-00020674. PR XX

XX (EVOL-) EVOLUTEC LTD. PA XX

XX Nuttall PA, Paesen GC, PT XX

XX DR WPI; 2001-257675/26. PT XX

PT Use of histacalain proteins for treating or preventing conjunctivitis, or for manufacturing a medicament for treating or preventing conjunctivitis, e.g. seasonal or perennial allergic conjunctivitis. PT XX

PS Claim 4, Page 5-6; 1999; English. XX

CC The present invention relates to the use of a histacalain protein for treating or preventing conjunctivitis. The present sequence is the histacalain protein FSH-BP1. The invention is particularly useful in the treatment of allergic or seasonal conjunctivitis. CC

CC Sequence 171 AA; XX

Query Match Best Local Similarity 37.5%; Pred. No. 7.6e-20; Score 282; DB 4; Length 171; Matches 66; Conservative 29; Mismatches 69; Indels 12; Gaps 8; PT XX

QY 31 PIWAHBELIGKQDAWKSISDQGSVTVLAKTYENDGWSWASQPKCQLQVQSTIERKEDY 90 CC

Db 3 PWDWEEAANGAHQPAWKSISKADTENVYVYKATKNDP-WGMIDTCVGMANDVNBDEK 61 CC

QY 91 TVTISVFTF-RNASSFPKIYVNTETWKAQVFOYQYKRNIALEQVGGGINITDILFIDGE 149 CC

Db 62 SIQARFLFMNADTMQF--AETKTVTAVENQGY-NRENAFVRYTEDS3QVFTDVIAVSD-D 117 CC

QY 150 LCDYVYVPNAD--QGCCEWVWKSKHRYKHWYDTCYTFVFNFCAKDRKTYDIFWBECK 202 CC

Db 118 NCDVIVYVPGTDGNSEGGYELWT-TDYYDNPANCANKFNEY-AGVRETRDVFSACT 170 CC

RESULT 10 XX

AAW7448 ID AAW7448 standard; protein; 200 AA. SQ Sequence 200 AA;

AAW37448; XX

XX 08-JUN-1998 (first entry) DT XX

DE Tick vasoactive amine binding protein 1 MS-HBPI. XX

KW Mal-specific vasoactive amine binding Protein 1; MS-HCPI; histamine; serotonin; assay; antihistamine; anti-inflammatory; insect bite; snake bite; scorpion bite; dermatitis; vaccine; transgenic animal; tick. KW XX

OS Rhipicephalus appendiculatus. XX

KEY Location/Qualifiers FT 1..18 FT /label= Sig\_peptide FT 79..81 FT /note= "Pasn is N-glycosylated" XX

RESULT 11 XX

AY18480 ID AY18480 standard; protein; 200 AA. XX

AC AY18480; XX

DT 06-AUG-1999 (first entry) DT XX

DB Histamine binding protein MS-HBPI. DB XX

XX Histamine binding protein; serotonin binding compound; inflammation; KW Histamine acid secretion; allergy; type I hypersensitivity reaction; KW asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; KW XX

PN WO9744451-A2. PN XX

XX 27-NOV-1997. PR XX

XX 19-MAY-1997; 97WO-GB001372. PR XX

XX Example 2; Fig 3; 44pp; English. XX

CC This protein comprises tick *Rhipicephalus appendiculatus* (Ra) novel male-specific histamine binding Protein 1 (MS-HBPI). Its amino acid sequence was deduced from a cDNA clone (see AAV00227) obtained from a salivary gland cDNA library. Female-specific HSP1 and HSP2 (see AAV37446-47) and a related protein, D-RE76 (see AAV37449) from *Dermacentor reticulatus*, were also identified. These novel vasoactive amine binding proteins (VABPs) can be expressed in host cells using e.g. a baculovirus expression system. They can be used: (i) to assay histamine (or other VA such as serotonin) in body fluids or cell culture supernatants, e.g. to monitor the effect of allergens; (ii) for binding VA, e.g. to remove histamine from blood, food, cell cultures etc.; (iii) as an antihistamine or anti-inflammatory agents, e.g. for treating scorpion or snake bites or dermatitis, or as a carrier for slow release of histamine-related compounds; (iv) in vaccines to protect against metazoan parasites, especially in animals; (v) as reagents for studying inflammation, involvement of VA in ulcer formation or the immune-response etc. VABPs provide a more sensitive assay for histamine than low-affinity antibodies currently used. They may also be more effective and safer than conventional antihistamines CC

CC Sequence 200 AA;

Query Match Best Local Similarity 34.5%; Pred. No. 4.7e-18; Score 265; DB 2; Length 200; Matches 69; Conservative 34; Mismatches 71; Indels 26; Gaps 10; Gaps PT XX

QY 3 MCQVLLITFVSAALATOETTSAKAGENPIWAHBELIGKQDAWKSISDQGSVTVLAKT 62 CC

Db 1 MKVLLIV- -LGAALCONADA- - - - -NPTWANEAKLGSYQDAWKSISQDQDNTRVYLAQ 51 CC

QY 63 TYENDGWSWASQPKCQLV- QBIERKEDDTVTSVFTFRN- SPIKYVNTETWKAQF 119 CC

Db 52 HQTD-GVWGBEFTCVSUTAEKIGKKLNATI- -LYKQKHLTDIJKESHETITWKAQD 106 CC

QY 120 YGKVNTRNAYEYQEVGGINIT- -DTLIFTDGEGLCDVYFPP- -NADQG-CELVWKKSHYR 173 CC

Db 107 Y--TTENGKIKETQGTRTQFEDVVFVFSDFYKNCVIFPKERGSDEGYELWNSEDKID 163 CC

QY 174 HFDYKTFVFNFCAKDRK 193 CC

Db 164 KIPDCCKFTMAYPAOOQKET 183 CC



Db	167 LEKFNEYAA-GLPVRDVYTSCL 188	Db	111 -NKENAIYQTEDGQVLTPLAFA- DNYVIVYALGPDGSGAGYELWA- -TDYTDVASC 166
RESULT 13		Qy	180 TPFVTFVFCAKDRKTYDIFNEECT 202
ID AAY18078	standard; protein; 190 AA.	:   :   :   :   :   :	:   :   :   :   :
XX		Db	167 LEKFNEYAA-GLPVRDVYTSCL 188
AC AAY18078;		AAB73262	
XX		ID AAB73262 standard; protein; 182 AA.	
DT 06-AUG-1999	(first entry)	XX	
XX		AC AAB73262;	
DE Histamine binding protein FS-HBPI.		XX	
XX		DT 15-MAY-2001 (first entry)	
KW Histamine binding protein; serotonin binding compound; inflammation; gastric acid secretion; allergy; type I hypersensitivity reaction; asthma; urticaria; allergic rhinitis; atopic dermatitis; food allergy; drug allergy; abnormal blood pressure; psychological disorder; vaccine; respiratory disease; coronary heart disease; cellular growth regulator; tissue repair; blood-sucking ectoparasite; therapy.		XX	
XX		DE Histacalain protein MS-HBPI.	
OS Rhipicephalus appendiculatus.		XX	
XX		AC MS-HBPI; histacalain protein; antiinflammatory; antiallergic; ophthalmological; allergic rhinitis.	
PN WO9927104-A1.		XX	
XX		OS Unidentified.	
PD 03-JUN-1999.		XX	
PF 25-NOV-1998;	98WO-GB003530.	PR 01-SEP-1999;	99GB-00020673.
XX		XX	
PR 26-NOV-1997;	97GB-0002546.	PA (EVOL-) EVOLUNEC LTD.	
PR 26-JUN-1998;	98GB-00013917.	XX	
XX		PA Nuttall PA, Paesen GC;	
PA (OFO-) OXFORD VACS LTD.		XX	
XX		PR 24-AUG-2000; 2000WO-GB003287.	
PT Nuttall PA, Paesen GC;		XX	
PT XX		PR 08-MAR-2001.	
PS WPI; 1999-357841/30.		XX	
XX		PS WPI; 2001-21851/22.	
PS Claim 1; Fig 1; 84pp; English.		XX	
XX		CC Use of histacalain proteins for treating or preventing allergic rhinitis, e.g. seasonal or perennial allergic rhinitis.	
PS This sequence is an example of a histamine or serotonin binding compound (A) of the invention. The compounds are useful for regulating the action of histamine and serotonin (e.g. inflammation and gastric acid secretion), the detection, quantification and removal of histamine or serotonin (in animals, plants, cell cultures, food materials, or humans) and in the treatment of various diseases and allergies (e.g. type I hypersensitivity reactions, urticaria, asthma, allergic rhinitis (hay fever), atopic dermatitis, insect bites and food and drug allergies, abnormal blood pressure, migraine, psychological disorders, respiratory disease, and coronary heart disease). Histamine may also be used to regulate cellular growth and tissue repair. The molecules may also be used as components of vaccines directed against blood-sucking ectoparasites		CC The present invention relates to a method for treating or preventing allergic rhinitis. The method involves employing a blood-feeding ectoparasite-derived (e.g. tick-derived) histacalain protein. The histacalain protein, is useful for treating or preventing allergic rhinitis, both seasonal and perennial allergic conjunctivitis	
XX		CC Sequence 182 AA;	
XX	Sequence 190 AA;	Qy 30 NPIWMAHESLIGQYDAWKSIDQGVSTVLAKEYTENDGGSWSQPKCQV-OBIEKE 87	Qy 1 NPPWANEAKIGSYQDAWKSIDQDQNRVYLAQATTD-GWVGBFTCVTAERIGK 59
Query Match 22.4%; Score 252; DB 2; Length 190; Best Local Similarity 33.5%; Pred. No. 8.7e-17; Mismatches 66; Indels 17; Gaps 8; Matches 68; Conservative 28; Mismatches 89; Indels 18; Gaps 8;	Db 1 MQLLUSLAFVJALASQVKA-----DKPWADBRANGEHQDVKHLQKLVBENTDILKA 52	Qy 88 EDYVUTSVFTERNAS-SPIKIVVNTIVTAKVAFQYKRNIALEYQVGGGLNIT-DPLI 144	Db 60 LNATI---LYKONKHLPIKESHTTIVKADY--TTENGIVKETQSTTQFEDVY 112
Qy 3 MQVVLITFVSAALATOQETSAKAGENPLWAHEBLLGKYDAWKSIDQGVSTVLAKEYTENDGGSWSQPKCQV-OBIEKE 62	Db 63 TYENDPGWSQSKCQLQVQSTERKEBDYTVTSVTFRMAASPIKIVVNTIVTAKVAFQY 122	Qy 145 FTDQELCDVYFYP--NADQG-CELVWKKSYKHADPKDTCIFUVNFCAKRKT 193	Db 113 PSDYKNCDVIFVPKERSGSDGDEYELWNSEDKDKIPDCCKPTMAYFAQQEKT 165
Qy 53 TYKNDP-VWGDFTFCVGAQNLNEDEKVNTEAMFMMNADTV-YQHPEKATPDKQY 110	Db 123 KMRNATIEYQVGGGANITDTLIFTDGEGLCDVYFYPNAD---QGCELMWVKSHKSYKHADPKDTC 179	RESULT 15	
Db AAB74290		ID AAB74290 standard; protein; 182 AA.	
Qy		XX	
		AC AAB74290;	

Search completed: March 9, 2004, 13:33:28  
Job time : 62 secs